

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 14:29:08 ; Search time 177 Seconds

(without alignments)
812.962 Million cell updates/sec

Title: US-10-077-435-1

Perfect score: 1478

Sequence: 1 MAMMEVQGGPSLIGOTCVLIV.....NEHLIDMDHASFCAFLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: uniprot_03:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 1478 | 100.0 | 281 | 1 TN10_HUMAN | P50591 homo sapien |
| 2 | 963 | 65.2 | 287 | 2 O8K3GO | O8K3GO ratu |
| 3 | 930 | 62.9 | 291 | 1 TN10_MOUSE | P50592 mus musculu |
| 4 | 809.5 | 54.8 | 304 | 2 Q7T1F2 | Q7T1F2 gallu |
| 5 | 577.5 | 39.1 | 299 | 2 Q6DHG9 | Q6DHG9 brachydantio |
| 6 | 334.5 | 22.6 | 317 | 2 Q7ZYX9 | Q7ZYX9 brachydantio |
| 7 | 307.5 | 20.7 | 287 | 2 Q90WT9 | Q90WT9 gallu |
| 8 | 305.5 | 20.7 | 214 | 2 Q9DDZ5 | Q9DDZ5 brachydantio |
| 9 | 291 | 19.7 | 63 | 2 Q6TSD9 | Q6TSD9 homo sapien |
| 10 | 267.5 | 18.1 | 318 | 1 TN11_PAT | O9ESE2 r tumor nec |
| 11 | 258.5 | 17.5 | 316 | 1 TN11_MOUSE | O35235 m tumor nec |
| 12 | 251.5 | 17.0 | 317 | 1 TN11_HUMAN | O14788 h tumor nec |
| 13 | 189.5 | 12.8 | 279 | 1 TNF6_MOUSE | P41047 mus musculu |
| 14 | 187 | 12.7 | 280 | 1 TNF6_CERTO | O9BDH1 cercocebus |
| 15 | 186 | 12.6 | 281 | 1 TNF6_HUMAN | P48823 homo sapien |
| 16 | 185 | 12.5 | 280 | 1 TNF6_MACFA | P63308 macaca fasc |
| 17 | 185 | 12.5 | 280 | 1 TNF6_MACMU | P63307 macaca mula |
| 18 | 185 | 12.5 | 280 | 1 TNF6_MACNE | P63306 macaca neme |
| 19 | 184.5 | 12.5 | 279 | 2 Q7TMV9 | Q7TMV9 mus musculu |
| 20 | 184 | 12.4 | 272 | 1 TNF5_CHICK | O918d8 gallu |
| 21 | 182 | 12.3 | 282 | 1 TNF6_PIG | O9BDA8 sus scrofa |
| 22 | 180 | 12.2 | 252 | 2 O8K3Y8 | O8K3Y8 mus musculu |
| 23 | 178.5 | 12.1 | 280 | 1 O8K1W5 | O8K1W5 felis silve |
| 24 | 177.5 | 12.0 | 278 | 1 TNF6_PAT | P63340 ratu |
| 25 | 175.5 | 11.9 | 169 | 2 Q9WV90 | Q9WV90 marmosa mon |
| 26 | 175 | 11.8 | 252 | 2 O8OY20 | O8OY20 mus musculu |
| 27 | 173 | 11.7 | 252 | 2 O8K3Y7 | O8K3Y7 ratu |
| 28 | 166 | 11.2 | 251 | 2 O8NPE9 | O8NPE9 homo sapien |
| 29 | 164 | 11.1 | 261 | 1 TNF5_BOVIN | P5149 bos tauru |
| 30 | 163.5 | 11.1 | 131 | 2 O6J3O6 | O6J3O6 canis fami |
| 31 | 160 | 10.8 | 174 | 1 TN15_HUMAN | O95150 homo sapien |

| | | | | | |
|----|-------|------|-----|--------------|--------------------|
| 32 | 159.5 | 10.8 | 240 | 1 TN14_HUMAN | O43557 homo sapien |
| 33 | 157 | 10.6 | 154 | 2 O8M19 | O8M19 macaca mula |
| 34 | 153.5 | 10.4 | 227 | 2 O7C203 | O7C203 cyprinu |
| 35 | 152.5 | 10.3 | 239 | 1 TN14_MOUSE | O9GYH9 mus musculu |
| 36 | 152 | 10.3 | 261 | 1 TNF5_CALA | O9BDH3 callithrix |
| 37 | 150.5 | 10.2 | 261 | 1 TNF5_AOTR | O9BDM3 aotus trivi |
| 38 | 149.5 | 10.1 | 260 | 1 TNF5_FELCA | O97605 felis silve |
| 39 | 149 | 10.1 | 241 | 2 O6U817 | O6U817 lateolabrax |
| 40 | 148 | 10.0 | 261 | 1 TNF5_CERTO | O96817 cercocebus |
| 41 | 148 | 10.0 | 261 | 1 TNF5_MACMU | P63304 macaca mula |
| 42 | 147.5 | 10.0 | 260 | 1 TNF5_CANFA | O97626 canis fami |
| 43 | 147.5 | 10.0 | 261 | 1 TNF5_HUMAN | P29965 homo sapien |
| 44 | 144.5 | 9.8 | 216 | 2 O70332 | O70332 mesocricetu |
| 45 | 143 | 9.7 | 261 | 1 TNF5_PIG | O95mg5 sus scrofa |

ALIGNMENTS

RESULT 1
ID TN10_HUMAN STANDARD; PRT; 281 AA.
AC P50591;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN Name=TNFSF10; Synonyms=APO2L, TRAIL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777113; DOI=10.1016/j.jbc.271.22.12687;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C.A., Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF family that induces apoptosis."
RT Immunol. 3:673-682(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96278649; PubMed=8663110; DOI=10.1074/jbc.271.22.12687;
RA Bhatti R.M., Masters S.A., Ruppert S., Donahue C.J., Moore A., Ashkenazi A.;
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family."
RT J. Biol. Chem. 271:12687-12690(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=12388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strussberg R.L., Fehlgold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stachelson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carinici P., Prange S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gumaratne P.H., Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W., Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 RX MEDLINE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5;
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ulicsch M., O'Connell M.,
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;
 RT "Triggering cell death: the crystal structure of Apopt1/TRA1L in a
 RT complex with death receptor 5.";
 RL Mol. Cell 4:563-571(1999).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RX PubMed=10542098; DOI=10.1038/19335;
 RA Morigkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Screaton G.R.;
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RT specificity in apoptotic initiation.";
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RX MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 RA Sung Y.C., Oh B.-H.;
 RT "2.8 Å resolution crystal structure of human TRAIL, a cytokine with
 RT selective antitumor activity.";
 RL Immunity 11:253-261(1999).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRA1LR1,
 CC TNFRSF10B/TRA1LR2, TNFRSF10C/TRA1LR3, TNFRSF10D/TRA1LR4 and
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRA1LR3, TNFRSF10D/TRA1LR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -1- COPACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 CC trimer.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung
 CC and prostate.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, U37518; AAC50332.1; -;
 DR EMBL, U57059; AAB01233.1; -;
 DR EMBL, BC037222; AAH3722.1; -;
 DR PDB, 1D0G; X-ray; A/B/D=114-281.
 DR PDB, 1D2Q; X-ray; A=114-281.
 DR PDB, 1D4V; X-ray; B=119-281.
 DR PDB, 1D66; X-ray; A=91-281.
 DR PDB, 1D03; X-ray; D/E/F/K/L=114-281.
 DR Genew; HGNC:11925; TNFSF10.
 DR H-InvDB; HIX0003863; -;
 DR MIM; 603598; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005102; F:receptor binding; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0006917; P:induction of apoptosis; TAS.
 DR GO; GO:0041122; P:positive regulation of I-kappaB kinase/NF-kappaB; IEP.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS50049; TNF_2; 1.
 KW 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;
 KW Transmembrane; Zinc.
 FT DOMAIN 1 17 Cytoplasmic (Potential).
 FT TRANSMEM 18 38 Signal-anchor for type II membrane
 FT protein (Potential).
 FT DOMAIN 39 281 Extracellular (Potential).
 FT METAL 230 230 Zinc.
 FT STRAND 123 127
 FT STRAND 149 150
 FT STRAND 163 165
 FT STRAND 167 170
 FT STRAND 171 172
 FT TURN 173 176
 FT STRAND 180 193
 FT TURN 198 199
 FT STRAND 205 213
 FT STRAND 220 228
 FT TURN 233 234
 FT STRAND 237 250
 FT TURN 252 253
 FT STRAND 255 260
 FT HELIX 263 265
 FT STRAND 266 267
 FT TURN 270 272
 FT STRAND 274 279
 SQ SEQUENCE 281 AA; 32509 MW; DDAAEF78DAAB2F6D CRC64;
 Query Match 100.0%; Score 1478; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred. No. 4,4e-113;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSIGQTCVLIVIFTVLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMMEVGGPSIGQTCVLIVIFTVLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYVDPNDEBSMSPCQVQVWQLRQIVRKMLIRTSEETITVQEKQONISPLVERGPO 120
 DB 61 DDSYVDPNDEBSMSPCQVQVWQLRQIVRKMLIRTSEETITVQEKQONISPLVERGPO 120
 QY 121 RVAAHITTRGSRNTLSSPNSKNEKALGRKINSWSSSGHSFSLNLRNGLVIHKG 180
 DB 121 RVAAHITTRGSRNTLSSPNSKNEKALGRKINSWSSSGHSFSLNLRNGLVIHKG 180
 QY 181 FYYIYSQTYFRQSEIKENTKNDKQVQIYKYTSYPPILMKSAARNSCKDAEYGLY 240
 DB 181 FYYIYSQTYFRQSEIKENTKNDKQVQIYKYTSYPPILMKSAARNSCKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 RESULT 2
 Q8K3G0 PRELIMINARY; PRT; 287 AA.
 AC Q8K3G0;
 DT 01-OCT-2002 (Trembl) 22, Created)
 DT 01-OCT-2002 (Trembl) 22, Last sequence update)
 DT 01-MAR-2004 (Trembl) 26, Last annotation update)
 DE TNF-related apoptosis inducing ligand.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxId=10116;
 RN NCB1_TaxId=10116;
 RP SEQUENCE FROM N. A.
 RC STRAIN=DA;
 RA Mueller A.M., Giegerich G.;
 RL EMBL, AY115578; AAM49797.1; -;
 DR EMBL, AY115578; AAM49797.1; -;
 DR HSP; P50591; ID20.
 DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005164; P: tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 287 AA; 32979 MW; CAAFSBD7C833FEC CRC64;

Query Match 65.2%; Score 963; DB 2; Length 287;
Best Local Similarity 67.7%; Pred. No. 8.5e-71;
Matches 189; Conservative 29; Mismatches 51; Indels 10; Gaps 3;

QY 9 GPSLQD---TCVLIVFTVLLQSLCAVATYVYFTNELKQMODKYSKGIACFLKEDSY 64
DB 9 GPSFQHFMTVITICVLLQVLLQALTVATVYMFNNEVQLQDNYSKIGLACFSKEDGDF 68
QY 65 WPDNEESNPSQWQKQQLQQLVKKILRTSEBTSTVQEQQINISPLVREGPQVAA 124
DB 69 WSTDEGLINRCLQVKKQLYQLIEVTLRTPEKTIPTVEKQLSTPPLRGRRPQVAA 128
QY 125 HITGTRGSNTLSPNSKNEKALGRKINSMESSRSGHSFLSNLHNGELVTHEKGFYI 184
DB 129 HITGTRGRNLLALPIKSKQKTLGQKITEMESSRSHSLNHYHLNGLVLYQDEGLYII 188
QY 185 YSQTYFRQGE--EIKENTKND---KQWQVYIKYTSYPPDPIILMKSARNSCMSKDAEY 238
DB 189 YSQTYFRQGEAKESKTVSKDGRIKQWQVYIKYTSYPPDPIILMKSARNSCMSREAYG 248
QY 239 LYSIYQGGIFELKENDRIFVSVTNEHLIMDHEASFGA 277
DB 249 LYSIYQGGIFELKENDRIFVSVTNEHLIMDHEASFGA 287

RESULT 3
TN10 MOUSE
ID TN10_MOUSE STANDARD; PRT; 291 AA.
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein).
GN Name=TNFsf10; Synonyms=trail;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8; Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C.A., Goodwin R.C.;
RT "Identification and characterization of a new member of the TNF family that induces apoptosis";
RT Immunol 3:673-682 (1995).
CC - FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1, TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and possibly also to TNFRSF1B/OPG. Induces apoptosis. Its activity may be modulated by binding to the decoy receptors TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF1B/OPG that cannot induce apoptosis.
CC - SUBUNIT: Homotrimer (By similarity).
CC - SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC - TISSUE SPECIFICITY: Widespread.
CC - SIMILARITY: Belongs to the tumor necrosis factor family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; U37522; AAC52345.1; -
DR HSSP; P50591; ID20.
DR MGD; MGI:107414; Tnfef10.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Apoptosis; Cytokine; Signal-anchor; Transmembrane.
FT DOMAIN 1 17 Cytoplasmic (Potential).
FT TRANSMEM 18 38 Signal-anchor for type II membrane protein (Potential).
FT DOMAIN 39 291 Extracellular (Potential).
FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 62.9%; Score 930; DB 1; Length 291;
Best Local Similarity 65.6%; Pred. No. 4.4e-68;
Matches 177; Conservative 37; Mismatches 50; Indels 6; Gaps 1;

QY 17 VLIVFTVLLQSLCAVATYVYFTNELKQMODKYSKGIACFLKEDSYWPDNEESNPS 76
DB 21 ICIVLQVLLQAVSAVATVYMFNNEVQLQDNYSKIGLACFSKEDGDFWDSIGILNRP 80
QY 77 CQWQKQQLQQLVKKILRTSEBTSTVQEQQINISPLVREGPQVAAHITGRSNTL 136
DB 81 CLQVKKQLYQLIEVTLRTPEKTIPTVEKQLSTPPLRGRRPQVAAHITGRSNTL 140
QY 137 SSPNSKNEKALGRKINSMESSRSGHSFLSNLHNGELVTHEKGFYIYQTYFRQGE- 195
DB 141 LPIKSKQKTLGQKITEMESSRSHSLNHYHLNGLVLYQDEGLYIIYQTYFRQGE- 200
QY 196 -----IKENTKNDKQWQVYIKYTSYPPDPIILMKSARNSCMSKDAEYGIYQGGIFEL 250
DB 201 DASKKVSQDKRTKQLQVLYIKYTSYPPDPIILMKSARNSCMSRDAEYGIYQGGIFEL 260
QY 251 KENDRIFVSVTNEHLIMDHEASFGAFLV 280
DB 261 KENDRIFVSVTNEHLIMDHEASFGAFLI 290

RESULT 4
Q7TIF2
ID Q7TIF2 PRELIMINARY; PRT; 304 AA.
AC Q7TIF2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Tumor necrosis factor related apoptosis inducing ligand.
GN Name=TRAIL;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OC NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: Spleen;
RA Sayed A.A., Horiiuchi H., Furusawa S., Matsuda H.;
RT "Molecular Cloning and Characterization of Chicken Tumor Necrosis Factor (TNF) Superfamily Ligands, CD30L and TNF-Related Apoptosis Inducing Ligand (TRAIL).";
RT J. Vet. Med. Sci. 66:643-650 (2004).
RL J. Vet. Med. Sci. 66:643-650 (2004).
EMBL; AB114678; BAC79267.1; -

RA Raha S.S., Loquejano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosack S.A., McEwen P.J., McKernan K.J., Malek J.A., Gnaratine P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Gilmour J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maier M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC044336; AAH44336.1; -.
 DR HSSP; P50591; ID20.
 DR ZFIN; ZDB-GENE-010801-1; tnfe101.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PSS0049; TNF_2; 1.
 SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DC9F CRC64;
 Query Match 22.6%; Score 334.5; DB 2; Length 317;
 Best Local Similarity 29.2%; Pred. No. 3.7e-19;
 Matches 83; Conservative 55; Mismatches 113; Indels 33; Gaps 8;
 QY 18 LIVITFVLQ--SLCVAVTVVYFT-----NELKQM--QDKYKSGIACFLKEDDSYWD 71
 DB 40 MVIIVVVLQIASTGLFVYLNMSLSQVSGVTEBLRCLGLNLVIGKQDIT--PEDLAQ 97
 QY 72 SNNSPCWQKWLRLQVLRLK-----ILRTSEETISTVOEKQNISPLVERGCP 120
 DB 98 LFGEFCMKLABEIKAYISKVTSIISKTLHAARTHTTSGSFMTTV-----NQ 150
 QY 121 RVAHAHITGRGSRNT-----LSSPNSKNEKALGRKINSWSSRGHSFLSNLHNGELV 175
 DB 151 RPSAHLTLSSASDNSRPGSDMHQPFDLHQSCRHPVHTW-ANKSFGAHLNNMTLTNGRLR 209
 QY 176 IHEKGFYIYSQTYFRF-QEELKENTKNDKQWQYIYKTSYDPDLLMKSNRNSQMSKD 234
 DB 210 VQDGRYVLYSQVYFRPSPSDSDSSVSHQVLCQCYKTKTSYLNPIQLKGVGTCKWAD 269
 QY 235 AEVGLYSIYQGIFFELKENDRIFVSVTNEHLIDMDHEASFGCAF 278
 DB 270 AEYALHSVYQGLFELRAGDEVFVSSTPTMYGGESSSYFCAF 313
 RESULT 7
 Q90MT9 PRELIMINARY; PRT; 287 AA.
 AC Q90MT9; 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE TNF-related apoptosis inducing ligand-like protein.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phaethonidae; Phaethonidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Briggham J.T., Johnson A.L.,
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY057941; AAL23702.1; -.
 DR HSSP; P50591; ID20.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR Pfam; PF00229; TNF; 1.
 DR PROSITE; PSS0049; TNF_2; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PSS0049; TNF_2; 1.
 SQ SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;
 Query Match 20.8%; Score 307.5; DB 2; Length 287;
 Best Local Similarity 32.3%; Pred. No. 5.3e-17;
 Matches 93; Conservative 46; Mismatches 110; Indels 39; Gaps 11;
 QY 18 LIVITFVLQ--SLCVAVTVVYFT-----NELKQM--QDKYKSGIACFLKEDDSYWD 66
 DB 8 LHAFLSLQLPLCTAPWMAEQTWSQALQNAFRLKAGSGSSBELRCLQLNQDQEG 67
 QY 67 PNDESM-NSPCWQKWLRLQVLRLK-----ILRTSEETI--STVOEKQ--NISL-YVERGP 119
 DB 68 SNLEELISNQC-----LKLANTIKAVVATVTEVVISRSVNEAOKSYFNISGQVATKTL 123
 QY 120 QVVAHI-----TGRGSRNTLSSPNSKNEKALGRKINSWSSRGHSFLSNLHLR 170
 DB 124 GKPASHLFRPQNPADGSSRRFNLIS-----QSCRHAIRWEDS-TISHLQNIYTR 175
 QY 171 NGEIVYHEKGFYIYSQTYFRFQEBIKENTKNDKQWQYIYKTSYDPDLLMKSNRNSC 230
 DB 176 DGRILVNAQKGYVYSQIYFRYSRDGAGARVSPVLQVCLNMTKTSYSGIILLKGVGTIC 235
 QY 231 WSKDAEGLYSIYQGIFFELKENDRIFVSVTNEHLIDMDHEASFGCAF 278
 DB 236 WAPAEVGLYHALYQGLFELKAGDELFFVSLSLAIDYSPAASYPCAF 283
 RESULT 8
 Q9DD25 PRELIMINARY; PRT; 214 AA.
 AC Q9DD25; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE TRAIL-like protein.
 GN Name=tnfsf101;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bobe J., Goetz F.W.,
 RT "Molecular cloning and expression of a TNF receptor and two TNF
 RT ligands in the fish ovary.";
 RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481 (2001).
 DR EMBL; AF250041; AAG47640.1; -.
 DR HSSP; P50591; ID20.
 DR ZFIN; ZDB-GENE-010801-1; tnfsf101.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PSS0049; TNF_2; 1.
 SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

| Query Match | Similarity | 20.7% | Score 305.5 | DB 2 | Length 214 |
|-------------|--|---|---------------|-----------|------------|
| Best Local | Similarity 37.6% | Pred. No. 5.3e-17 | | | |
| Matches | 62 | Conservative 37 | Mismatches 59 | Indels 7 | Gaps 3 |
| Qy | 120 | QVAAHITGTRGRSNT-----LSSPNSKNEKALGRIKINSWESSRSGHSFLSNILRNGEL | 174 | | |
| Db | 47 | QPSAHITLTSASDNRSPQSDWHQPOFDLQSCRHPVHTW-ANKSFGAHLVYMTLTNGRL | 105 | | |
| Qy | 175 | VIHERGFIYIYQTYFRF-QEIKENTKNDQMQYIKYISYPPILIMKSAARNSCMK | 233 | | |
| Db | 106 | RVPDGRFYLLSYQYFRYRSPSDSQSSVSHQLVQCIKTKISYLYNPIDLKGVGTGCPAP | 165 | | |
| Qy | 234 | DAEYGLSYIYOGGIFELKENDRIFFYATVNEHIDMDHEASFGCAF | 278 | | |
| Db | 166 | DAEYALHSVYOGGLFELRAGDEVFVSVPMTWVEDESSYTGAF | 210 | | |
| RESULT 9 | | | | | |
| Q6JSD9 | PRELIMINARY; | PRT; | 63 AA. | | |
| AC | Q6JSD9 | | | | |
| DT | 05-JUL-2004 (TREMBlrel. 27, Created) | | | | |
| DT | 05-JUL-2004 (TREMBlrel. 27, Last sequence update) | | | | |
| DT | 05-JUL-2004 (TREMBlrel. 27, Last annotation update) | | | | |
| DE | Chemokine tumor necrosis factor ligand superfamily member 10 (Fragment). | | | | |
| GN | Name=TNFSF10; | | | | |
| OC | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RP | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | Tissue=Lung carcinoma; | | | | |
| RA | Poivi A., Ruusaari S., Vendelin J., West A., Saarikko I., | | | | |
| RA | Reinikainen A., Hollmen J., Laitinen T., Mannila H., Laheesmaa R., | | | | |
| RA | Kere J.; | | | | |
| RL | Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; AY315279; AAR16184.1; -. | | | | |
| FT | NON TER | | | | |
| SO | SEQUENCE 63 AA; 7638 MW; 8F0C7936DA5A5A66 CRC64; | | | | |
| Query Match | 19.7% | Score 221 | DB 2 | Length 63 | |
| Best Local | Similarity 100.0% | Pred. No. 1.7e-16 | | | |
| Matches | 52 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| Qy | 39 | TNELKQMDKXKSGIACFLKEDDSYNPNDSESNNSFCWQYKQOLRLVVK | 90 | | |
| Db | 1 | TNELKQMDKXKSGIACFLKEDDSYNPNDSESNNSPCWQYKQOLRLVVK | 52 | | |
| RESULT 10 | | | | | |
| ID | TN11_RAT | STANDARD; | PRT; | 318 AA. | |
| AC | QSESE2; G91Z19; | | | | |
| DT | 28-FEB-2003 (Rel. 41, Created) | | | | |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | | | |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) | | | | |
| DE | Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF). | | | | |
| GN | Name=Trnfsl1; Synonyms=Opgl, Rankl, Trance; | | | | |
| GN | Rattus norvegicus (Rat). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | | | |
| OX | NCBI_TaxID=10116; | | | | |
| RP | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | Tissue=Tibial bone; | | | | |
| RC | MEDLINE=20540945; PubMed=11092398; | | | | |
| RA | Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S., | | | | |

| | |
|-----------------------|--|
| RA | Zheng M.H.; |
| RT | "Cloning, sequence and functional characterization of the rat |
| RL | homologue of receptor activator of NF- κ B ligand."; |
| J. | Bone Miner. Res. 15:2178-2186(2000). |
| [2] | |
| RN | SEQUENCE OF 266-318 FROM N.A. |
| RP | STRAIN=Fischer 344; |
| RC | Ogden P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savas A., |
| RA | Satadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y., |
| RA | Marks S.C. Jr.; |
| RT | "Evidence that the rat osteopetrotic mutation toothless (tl) is not in |
| RT | the TNFRSF11 (TNFCE, RANKL, ODF, OPGL) gene"; |
| RL | Int. J. Dev. Biol. 45:853-859(2001) |
| CC | -I- FUNCTION: Cytokine that binds to TNFRSF11B/ODG and to |
| CC | TNFRSF11A/RANK. Osteoclast differentiation and activation factor. |
| CC | Augments the ability of dendritic cells to stimulate naive T-cell |
| CC | proliferation. May be an important regulator of interactions |
| CC | between T cells and dendritic cells and may play a role in the |
| CC | regulation of the T cell-dependent immune response. May also play |
| CC | an important role in enhanced bone-resorption in humoral |
| CC | hypercalcaemia of malignancy. |
| CC | -I- SUBUNIT: Homotrimer (By similarity). |
| CC | -I- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By |
| CC | similarity). |
| CC | -I- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues. |
| CC | -I- PFM: The soluble form derives from the membrane form by |
| CC | proteolytic processing (By similarity). |
| CC | -I- SIMILARITY: Belongs to the tumor necrosis factor family. |
| CC | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - |
| CC | the European Bioinformatics Institute. There are no restrictions on its |
| CC | use by non-profit institutions as long as its content is in no way |
| CC | modified and this statement is not removed. Usage by and for commercial |
| CC | entities requires a license agreement (See http://www.jeb-sib.ch/announce/ |
| CC | or send an email to license@sib-sib.ch). |
| CC | |
| DR | EMBL; AF187319; AAC17031.1; -; |
| DR | EMBL; AF425669; AAL23963.1; -; |
| DR | HSSP; O35235; IUTZ. |
| DR | RCD; 620784; Tntsf11. |
| DR | InterPro; IPRO06052; TNF family. |
| DR | InterPro; IPRO08983; TNF_like |
| DR | InterPro; IPRO0536; TNF_subf. |
| DR | Pfam; PF00229; TNF; 1. |
| DR | ProDom; PD002012; TNF_subf; 1. |
| DR | SMART; SM00207; TNF; 1. |
| DR | PROSITE; PS00251; TNF_1; FALSE_NEG. |
| DR | CytoKine; Differentiation; Glycoprotein; Receptor; Signal-anchor; |
| KW | Transmembrane. |
| FT | CHAIN 1 318 |
| FT | |
| FT | CHAIN 141 318 |
| FT | |
| FT | DOMAIN 1 47 |
| FT | TRANSMEM 48 68 |
| FT | |
| FT | DOMAIN 69 318 |
| FT | SITE 140 141 |
| FT | CARBHYD 199 199 |
| FT | CARBHYD 264 264 |
| FT | CONFLICT 317 317 |
| SO | SEQUENCE 318 AA; 35370 MW; 4B874AD706AD098F CRC64; |
| | |
| Query Match | 18.1%; Score 267.5; DB 1; Length 318; |
| Best Local Similarity | 27.3%; Pred. No. 1.2e-13; |
| Matches | 82; Conservative 55; Mismatches 106; Indels 57; Gaps 11; |
| 0y | 10 PSIGQTCVLLIVIFVLTLQSICVAATYVYFNTELKOMDKYSKGIACF-----LKED--- 61 |
| D0 | 43 PAASRPFMLLDLGICAGVCISIALFLFYFAQMD--PNRSISBSTRCFYAIRLRREVTGL 100 |

QY 62 -DSYWDPNDEESMNSPCQVQKQLQVLKMTLRTSEITSTVOEKQONISPLVERGPO 120
 DB 101 QDSTLESEDTXALPDSCKRMKAFO-----GAVQRELOHIV-----GPO 139
 QY 121 R---VAAHITGT-----RGRS-----NTLSPNSKNEKKALGRKINSMESSRSGH 161
 DB 140 RPSGVPAMMEGSLDVARRGKEADPFALHTINADIPESGSKVL-----SSWYHDR-CW 194
 QY 162 SFLSNLHLRNGELVHIEKGFYIYSQTYFRQOEIKENTKDKQVQVYIKYT-SYDPDI 220
 DB 195 AKISNWTLSNGKLRVQODGFYLLVYANICFRHNETSGSVADYLDQMVVYVXTSIRKIPSSH 254
 QY 221 LLMKARNSCWAKDEYGLYSIYOGGIFPLKENDRIFVSVTMELHLDHMSFPFGALY 280
 DB 255 NLMKGGSTKNWSGNSSEFHFYSINVGGFFLARGEEISVQVSNPSLDDPDQATYFGAFKY 314

RESULT 11
 TN11_MOUSE STANDARD; PRT; 316 AA.
 AC 035235; 035306; 09JUK8; 09JUK9; 09RIY0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
 (OCIF).
 DE (OCIF).
 GN Name=Trsf11; Synonyms=OPGL, RANKL, Trance;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hybridoma; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
 RX MEDLINE=97460112; PubMed=97460112; PubMed=97460112; Chao M.,
 RA Wong B.R., Rho J., Arton J., Robinson E., Orlinick J., Chao M.,
 RA Kalachikov S., Cayan E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thymic lymphoma; PubMed=9367155; DOI=10.1038/36593;
 RX MEDLINE=98032977; PubMed=9367155; PubMed=9367155; Dougall W.C.,
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometako M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
 RX MEDLINE=98227661; PubMed=9568710; PubMed=9568710; Lacey D.L.,
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott C., Scully S., Hsu H.,
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyle W.J.;
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
 RT differentiation and activation.";
 RL Cell 93:165-176(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow stroma; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
 RX MEDLINE=98188248; PubMed=9520411; PubMed=9520411; Yasuda H.,
 RA Yasuda H., Shima N., Nakegawa N., Yamaguchi K., Kitosaki M.,
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,

RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
 RT "Osteoclast differentiation factor is a ligand for
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
 RT to TRANCE/RANKL.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=129;
 RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
 RA Ueda M., Higashio K.;
 RT "Cloning and characterization of the gene encoding mouse osteoclast
 RT differentiation factor.";
 RL Gene 230:121-127(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
 RT "Determination of three isoforms of the receptor activator of nuclear
 RT factor-kappaB ligand and their differential expression in bone and
 RT thymus.";
 RL Endocrinology 142:1419-1426(2001).
 RN [7]
 RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
 RX MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
 RA Lum L., Wong B.R., Jostein R., Becherer J.D., Erdjument-Bromage H.,
 RA Schindler J., Tempst P., Choi Y., Blobel C.P.;
 RT "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
 RT converting enzyme-like protease in shedding of TRANCE, a TNF family
 RT member involved in osteoclastogenesis and dendritic cell survival.";
 RL J. Biol. Chem. 274:13613-13616(1999).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
 RX MEDLINE=21464816; PubMed=11581298;
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
 RT of receptor-ligand specificity.";
 RL J. Clin. Invest. 108:971-979(2001).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
 RX MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at
 RT 2.2-A resolution.";
 RL J. Biol. Chem. 277:6631-6636(2002).
 RN [10]
 RP TNPFRS11B/OPG and to
 CC TNPFRS11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcaemia of malignancy.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUGCELLULAR LOCATION: Type II membrane protein and secreted
 CC (isoforms 1 and 2). Cytoplasmic (isoform 3).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O35235-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O35235-2; Sequence=VSP_006449;
 CC Name=3;
 CC IsoId=O35235-3; Sequence=VSP_006448;
 CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
 CC but not in nonlymphoid tissues and is abundantly expressed in T
 CC cells but not in B cells. A high level expression is also seen in
 CC the trabecular bone and lung.
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing. The cleavage may be catalyzed by
 CC ADAM17. A further shorter soluble form was observed.
 CC -1- DISEASE: Deficiency in Tnfrsf11 results in failure to form lobulo-

CC alveolar mammary structures during pregnancy, resulting in death
 CC of newborns. Transc-deficient mice show severe osteopetrosis, with
 CC no osteoclasts, marrow spaces, or tooth eruption, and exhibit
 CC profound growth retardation at several skeletal sites, including
 CC the limbs, skull, and vertebrae and have marked chondrocytasia,
 CC with thick, irregular growth plates and a relative increase in
 CC hypertrophic chondrocytes.
 CC
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF011370; AAC71061.1; -
 CC EMBL: AF013048; AAB86812.1; -
 CC EMBL: AF053713; AAC40113.1; -
 CC EMBL: AB008426; BAA25425.1; -
 CC EMBL: AB022039; BAA36970.1; -
 CC EMBL: AB022037; BAA36970.1; JOINED.
 CC EMBL: AB022038; BAA36970.1; JOINED.
 CC EMBL: AB032772; BAA97257.1; -
 CC EMBL: AB032772; BAA97258.1; -
 CC EMBL: AB036798; BAA97259.1; -
 CC PDB: 1IOA; X-ray; A/B/C=157-316.
 CC PDB: 1UTZ; X-ray; X/Y/Z=244-316.
 CC WGD; MG:1100089; Tntf11.
 CC GO: GO:0005155; F:protein binding; IPI.
 CC GO: GO:0042804; P:protein homooligomerization activity; IDA.
 CC GO: GO:0045453; P:bone resorption; IDA.
 CC GO: GO:0009887; P:organogenesis; IMP.
 CC GO: GO:0001503; P:osteification; IMP.
 CC InterPro: IPR006052; TNF family.
 CC InterPro: IPR008983; TNF like.
 CC InterPro: IPR003636; TNF subf.
 CC Pfam: PF00229; TNF; 1.
 CC ProDom: PD002012; TNF_subf; 1.
 CC SMART; SM00207; TNF; 1.
 CC PROSITE; PS00251; TNF_1; FALSE_NEG.
 CC PROSITE; PS0049; TNF_2; 1.
 CC 3D-structure: Alternative splicing; Cytokine; Differentiation;
 CC Direct protein sequencing; Glycoprotein; Receptor; Signal-anchor;
 CC Transmembrane.
 CC
 CC CHAIN 1 316 Tumor necrosis factor ligand superfamily
 CC member 11, membrane form.
 CC CHAIN 139 316 Tumor necrosis factor ligand superfamily
 CC member 11, soluble form.
 CC DOMAIN 1 48 Cytoplasmic (Potential).
 CC TRANSMEM 49 69 Signal-anchor for type II membrane
 CC protein (Potential).
 CC DOMAIN 70 316 Extracellular (Potential).
 CC SITE 138 139 Cleaveage.
 CC CARBOHYD 197 197 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 262 262 N-linked (GlcNAc...) (Potential).
 CC VARSPLIC 1 117 Missing (in isoform 3).
 CC VARSPLIC 14 44 /FTId=VSP 006448.
 CC VARSPLIC 14 44 SSBEMSGGVPHGELHAPAPAPAPPA -> TP (in
 CC isoform 2).
 CC FTId=VSP 006449.
 CC G -> D (in Ref. 2).
 CC Missing (in Ref. 5).
 CC
 CC CONFLICT 99 99
 CC STRAND 141 143
 CC STRAND 164 169
 CC TURN 171 172
 CC STRAND 181 182
 CC STRAND 186 187
 CC TURN 191 192
 CC STRAND 194 196
 CC STRAND 198 201

FT TURN 202 203
 Query Match 17.5%; Score 258.5; DB 1; Length 316;
 Best Local Similarity 26.4%; Pred. No. 6.3e-13;
 Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
 QY 10 PSLGQTCVLIYFYVLLSLCAVATYVYFTNELKOMQDKYSGSLAC-----LKEDSY 64
 DB 43 PAASRSMFLALGLGLGVVCSIALFLYFRQMD--PNRISDSHTRCYRILRLHENG 100
 QY 65 MDP--NDESNSSPCOWKQQLRQLVRGMILRTSEBETISTYOEKOQNTSPL----- 113
 DB 101 QDSTLESBDTLPDSCKRKKQAFQAVQK-----ELQHYGPQFSGAPAMM 146
 QY 114 -----VERGFORVA--AHITGRGNTLSPNSKNEKALGRKINSMESSRSGHFLS 165
 DB 147 EGSWLDVNRQKPEAQPFALHT-----INAAISPGSHKVTL-----SSWYHDR-GMAKIS 196
 QY 166 NMLHNGELVTHKEGFYITISQTFRFOEELKENTKDKQVQIYKKT-SYDPIILMK 224
 DB 197 NMTLSNGRLRVQDGFYLYANICFRHETSGSVPTDYLQLMVYVYKTSIKIPSSHNLMK 256
 QY 225 SARNSCWKDAEYGLYSYVGIGIFELKENDRIFVSVTNEHLIDMDHEASFGAFV 280
 DB 257 GGSTNMGSGNSBFHFIYINVGFFKLRAGEETISGVNSPLDDPDQATYFGAFKV 312
 RESULT 12
 ID TN11_HUMAN STANDARD. PRT. 317 AA.
 AC 014788; 014723; 096Q17; 09P203;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 DE differentiation factor) (ODF).
 GN Name=TNFSF11; Synonyms=OPGL, RANKL, TRANCE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=bone marrow, and Peripheral blood;
 RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougan W.C.,
 RA Tometsko W.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Galibert L.;
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RA and dendritic-cell function.";
 RL Nature 390:175-179 (1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph node;
 RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
 RA Lacey D.L., Tims E., Tan H.-L., Kelley M.J., Duncan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Ali A., Qian Y.-X.,
 RA Kautman S., Sirois I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyle W.J.;
 RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast
 RA differentiation and activation.";
 RL Cell 93:165-176 (1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RA Ikeda T., Kuroyama H., Hirokawa K.;
 RT "Determination of human RANKL isoforms.";
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 73-317 FROM N.A.
 RC TISSUE=Thymocytes;

RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
 RA Wong B.R., Rho J., Aron J., Robinson E., Orlicki J., Chao M.,
 RA Kalachikov S., Cayan E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates C-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [5].
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Tongue;
 RX MEDLINE=20175237; PubMed=10708588; DOI=10.1006/brc.2000.2314;
 RA Nagai M., Kyakumoto S., Sato N.;
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA
 RT encoding a secreted form of ODF/TRANCE that induces osteoclast
 RT formation.";
 RL Biochem. Biophys. Res. Commun. 269:532-536(2000).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
 CC secreted (isoform 2). A soluble form of isoform 1 arises by
 CC proteolytic processing (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O14788-1; Sequence=Displayed;
 CC Name=2; Synonyms=SOD5;
 CC IsoId=O14788-2; Sequence=VSP_006447;
 CC Name=3;
 CC IsoId=O14788-3; Sequence=VSP_006446;
 CC -1- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
 CC spleen, peripheral blood leukocytes, bone marrow, heart, placenta,
 CC skeletal muscle, stomach and thyroid.
 CC -1- INDUCTION: Up-regulated by T cell receptor stimulation.
 CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing (By similarity). The cleavage may be
 CC catalyzed by ADAM17.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; AF019047; AAB86811.1; -;
 CC EMBL; AF053712; AAC39731.1; -;
 CC EMBL; AB064269; BAB79694.1; -;
 CC EMBL; AB061227; BAB71768.1; -;
 CC EMBL; AB064270; BAB79695.1; -;
 CC EMBL; AF013171; AAC51762.1; -;
 CC EMBL; AB037599; BAA90488.1; -;
 CC HSSP; O35235; LUTZ.
 CC Genew; HGNC:11926; TNFRSF11.
 CC MIM; 602642; -;
 CC GO; GO:0005576; C:extracellular; NAS.
 CC GO; GO:0005887; C:integral to plasma membrane; NAS.
 CC GO; GO:0005164; P:tumor necrosis factor receptor binding; NAS.
 CC GO; GO:0006955; P:immune response; NAS.
 CC GO; GO:0030316; P:osteoclast differentiation; NAS.
 CC InterPro; IPR006052; TNF_family.
 CC InterPro; IPR008963; TNF_like.
 CC InterPro; IPR003636; TNF_subf.
 CC Pfam; PF00229; TNF_1.
 CC ProDom; PD002012; TNF_subf; 1.

DR SMART; SMO0207; TNF; 1.
 DR PROSITE; PS00251; TNF_2; 1. FALSE_NEG.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Alternative splicing; Cytokine; Differentiation; Glycoprotein;
 KW Receptor; Signal-anchor; Transmembrane.
 FT CHAIN 1 317 Tumor necrosis factor ligand superfamily
 FT member 11, membrane form.
 FT CHAIN 140 317 Tumor necrosis factor ligand superfamily
 FT member 11, soluble form (By similarity).
 FT DOMAIN 1 47 Cytoplasmic (Potential).
 FT TRANSMEM 48 68 Signal-anchor for type II membrane
 FT protein (Potential).
 FT DOMAIN 69 317 Extracellular (Potential).
 FT SITE 139 140 Cleavage (By similarity).
 FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 198 198 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 1 47 Missing (in isoform 3).
 FT VARSPLIC 1 73 Missing (in isoform 2).
 FT VARSPLIC 1 73 Missing (in isoform 2).
 FT CONFLICT 194 194 A -> G (in Ref. 4).
 FT SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;
 SQ SEQUENCE
 Query Match 17.0%; Score 251.5; DB 1; Length 317;
 Best Local Similarity 24.1%; Pred. No. 2.4e-12;
 Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;
 QY 10 PSLGQTCVLIIVFTVLQSLCYATVYVFMELKMDKYSAGIACF-----LKED--- 61
 DB 42 PAASRSMFVALGLGLGVQVCSVALFFYFRQMD--PRISIDGTHCYIRLIRHENDP 99
 QY 62 -DSYNDPNDDESMNSPCQVQK-----QRLQVVRKMLIRTSBETI-----STVQEQ 107
 DB 100 QDTLESQDTKLIIPSCRIKQAFQGAQVQKELQHVQSGCHTAAKAMVQGSGLDAKSK 159
 QY 108 QNISPLVERGEPQVRAAHITGRGRSNTLSPNSKREKALGRKINSWSSRSRGSPLSNTL 167
 DB 160 LEAGF-----AHLT-----INATDIPSGSHKXSL-----SWMHDR-GMAKISGM 199
 QY 168 HLRNGLVIERKGPYYITSQYFRPOEIKENTKDKQMOVIYTYT-SYDPILLMKSA 226
 DB 200 TFSNGKLIYNQDGFYLVANICFRHHTSGDLATEYLQIMVYVTSIKIPSSHTLMKGG 259
 QY 227 RNSCKSAEYGLVSIYGGIFELKENDRIPVSVNHEHLDMDHSAFPGALV 280
 DB 260 STKYSWSEFHFYSINVGFPKLSGSEISLEVSNSLDDPDQATYFGAKV 313
 RESULT 13
 TNF6_MOUSE STANDARD; PRT; 279 AA.
 ID TNF6_MOUSE
 AC P41047; Q61217; Q9R1P2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
 DE ligand).
 GN Name=tnf6; Synonyms=APTLIG1, Fasl, gld;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX MEDLINE=94185175; PubMed=7511063; DOI=10.1016/0092-8674(94)90375-1;
 RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
 RA Suda T., Nagata S.;
 RT "Generalized lymphoproliferative disease in mice, caused by a point
 RT mutation in the Fas ligand.";
 RL Cell 76:969-976(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
 RC STRAIN=C57BL/6;

RX MEDLINE=9538076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016-8;
 RA Peltsch M.J., Tschopp J.J.;
 RT "Comparative molecular modelling of the Fas-ligand and other members
 of the TNF family.";
 RL Mol. Immunol. 32:761-772(1995).
 CC [3]
 RN SEQUENCE FROM N.A. (ISOFORM FASL).
 RP MEDLINE=95196085; PubMed=7889405; DOI=10.1016/1074-7613(94)90106-6;
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
 RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
 RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF
 family gene cluster.";
 RL Immunity 1:131-136(1994).
 CC [4]
 RN SEQUENCE FROM N.A. (ISOFORM FASL).
 RP STRAIN=BALB/c;
 RA Fenner M.H., Shioda T., Iseelbacher K.J.;
 RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two
 amino acids.";
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 CC [5]
 RN SEQUENCE FROM N.A. (ISOFORM FASL).
 RP STRAIN=C3H; TISSUE=Spleen;
 RA MEDLINE=20021694; PubMed=10552956;
 RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,
 RA Camarile L., Migliorati G., Delfino D.V., Riccardi C.;
 RT "Cloning and expression of a short Fas ligand: a new alternatively
 spliced product of the mouse Fas ligand gene.";
 RL Blood 94:3456-3467(1999).
 CC [6]
 RN CHARACTERIZATION OF VARIANT GLD.
 RP MEDLINE=96091792; PubMed=7495745;
 RA Hahne M., Peitsch M.C., Irmeler M., Schroeter M., Lowin B.,
 RA Roussseau M., Bron C., Renno T., French L., Tschopp J.;
 RT "Characterization of the non-functional Fas ligand of gld mice.";
 RL Int. Immunol. 7:1381-1386(1995).
 CC [7]
 RN VARIANTS ALA-184 AND GLY-218.
 RP STRAIN=BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, NZW, and
 RC SJL;
 RA MEDLINE=97268671; PubMed=9108079; DOI=10.1073/pnas.94.8.3914;
 RA Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,
 RA Yagita H.;
 RT "Polymorphism of murine Fas ligand that affects the biological
 activity.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF6/Fas, a receptor that
 transduces the apoptotic signal into cells. May be involved in
 cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/Fas-mediated apoptosis may have a role in the induction of
 peripheral tolerance, in the antigen-stimulated suicide of mature
 T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3
 modulates its effects (by similarity).
 CC -1- SUBUNIT: Homotrimer (Probable).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Isoform FASL);
 CC Secreted (Isoforms FASL and FASLS).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=FasL;
 CC IsoId=P41047-1; Sequence=Displayed;
 CC Name=FASLS;
 CC IsoId=P41047-2; Sequence=VSP_006445;
 CC -1- PTM: The soluble form derives from the membrane form by
 proteolytic processing (By similarity).
 CC -1- DISEASE: A deficiency in this protein is the cause of generalized
 lymphoproliferation disease phenotype (gld). Gld mice present
 lymphadenopathy and autoantibody production. The phenotype is
 recessively inherited.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL, U06948; AAA17800.1; -
 CC EMBL, U10984; AAA19778.1; -
 CC EMBL, S76752; AAB33780.1; -
 CC EMBL, U58995; AAB02915.1; -
 CC EMBL, AF119335; AAD52106.1; -
 CC PIR, A53062; A53062.
 CC HSP, P50581; I2D66.
 CC MGJ, MGJ:99255; TNFef6.
 CC InterPro; IPR008064; Fas ligand.
 CC InterPro; IPR006053; TNF_abc.
 CC InterPro; IPR006052; TNF_family.
 CC InterPro; IPR008983; TNF_like.
 CC InterPro; IPR003636; TNF_subf.
 CC Pfam; PF00229; TNF_1.
 CC PRINTS; PR01681; FASLIGAND.
 CC PRODOM; PD002012; TNF_subf.1.
 CC PROSITE; PS00251; TNF_1.1.
 CC PROSITE; PS0049; TNF_2.1.
 CC Alternative splicing; Apoptosis; Disease mutation;
 CC Glycoprotein; Polymorphism; Signal-anchor; Transmembrane.
 CC CHAIN 1 279
 FT CHAIN 128 279
 FT DOMAIN 1 78
 FT TRANSMEM 79 100
 FT DOMAIN 101 279
 FT DOMAIN 4 69
 FT SITE 127 128
 FT DISULFID 200 231
 FT CARBOHYD 117 117
 FT CARBOHYD 182 182
 FT CARBOHYD 248 248
 FT CARBOHYD 258 258
 FT VARSPLIC 1 210
 FT VARIANT 184 184
 FT VARIANT 218 218
 FT VARIANT 273 273
 FT SEQUENCE 279 AA; 31442 MW; 3797282728E0A1CA CRC64;
 Query Match 12.8%; Score 189.5; DB 1; Length 279;
 Best Local Similarity 25.8%; Pred. No. 2.5e-07;
 Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;
 QY 83 QLRQVLRKMLRTSETISTVOEKQONISPIVREKGPQVAAHITGSGRSNTLSSPSRK 142
 DB 111 ELREFTNOSL-----KISSPEKQIANPSTSEKKEPSSV-AHLTG-----NPISR 154
 QY 143 NEKALGRKINSWESSRSGHSPLSNLHLRNGELVIHEKGFYYISQTYRPFQEEIKENTKN 202
 DB 155 SLPL-----EWEDT-YGTALISGVKKYKGGVLINETGLVFPYSKYVPRGQ-----SCN 201
 QY 203 DKQWQYIY-KYTSIPDPILMKSR-NSCWSKDAEYGLYSTYOGIEFLKENDRIFFSV 260
 DB 202 NQPLNHKKYMYRNSKYPEDLVLMEEKRLNYCTT--QGIWAHSYLGAVNLTSADHLVYNI 259
 QY 261 TNEHLIDMDEASPFQGA 278
 DB 260 SOLSLINFEBSKTFPGLY 277

```

RESULT 14
TNF6_CERTO STANDARD: PRT: 280 AA.
ID TNF6_CERTO
AC Q9BDN1
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
   (CD95L protein).
GN Name=TNFRSF6; Synonyms=CD95L, FASL;
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
RA Villinger F., Boeslik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
   Fae/Fas ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328(2001).
CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
   transduces the apoptotic signal into cells. May be involved in
   cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
   peripheral tolerance, in the antigen-stimulated suicide of mature
   T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
   modulates its effects (By similarity).
CC -1- SUBUNIT: Homotrimer (Probable).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
   similarity).
CC -1- PTM: The soluble form derives from the membrane form by
   proteolytic processing (By similarity).
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation-
   CC the European Bioinformatics Institute. There are no restrictions on its
   use by non-profit institutions as long as its content is in no way
   modified and this statement is not removed. Usage by and for commercial
   entities requires a license agreement (see http://www.embnet.ch/announce/
   or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: AF344847; AK37606.1; -.
DR HSSP: P50591; 1DQ0.
DR InterPro: IPR008064; Fae ligand.
DR InterPro: IPR006053; TNF_abc.
DR InterPro: IPR006052; TNF_family.
DR InterPro: IPR008983; TNF_like.
DR InterPro: IPR003636; TNF_subf.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01681; FASLIGAND.
DR PRINTS: PR01234; TNFCROSISCT.
DR PRODOM: PP002012; TNF_subf; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
KW Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
FT CHAIN 1 280 Tumor necrosis factor ligand superfamily
FT CHAIN 1 280 member 6, membrane form.
FT CHAIN 1 280 Tumor necrosis factor ligand superfamily
FT DOMAIN 1 80 member 6, soluble form (By similarity).
FT TRANSMEM 81 101 Cytoplasmic (Potential).
FT DOMAIN 102 280 Protein-anchor for type II membrane
FT DOMAIN 4 69 Extracellular (Potential).
FT SITE 45 64 Pro-rich.
FT SITE 128 129 Poly-Pro.
FT DISULFID 201 232 Cleavage (By similarity).
FT 201 232 Potential.

```

```

FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 249 249 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 280 AA; 31407 MW; 729EAC067BD398 CRC64;
Query Match 12.7%; Score 187; DB 1; Length 280;
Best Local Similarity 22.1%; Pred. No. 4e-07;
Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;
QY 4 MEVGGSPSLGQTCVIVIFETVLQSLCVAIVYVFTNLKQMDKYSKGIACFLKEDS 63
DB 70 LKRRNHNSTG-LCLLMFPMVLVALVGGLGMPQLFHQKELAE-----LRESTD 118
QY 64 WYDPNDESNMSPCQVQKQRLQVLKRLTSEETITVQKQNIPLVREGRPQVFA 123
DB 119 -----QKTHASLKLQICHPS-PEKKEQKRV 145
QY 124 AHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLRNGELVHEKGFY 183
DB 146 AHLTG-----KPNRSMPD-----EWEDT-YGIVLISGVYKKGGLVINEGLYF 189
QY 184 IYSCYFRFQREIKENTKNDKQMYIY-KTYSYDPILMKSNANSCMSDAEYGLYSI 242
DB 190 VYSKYVFFRQ-----SCTNLPLSHKYVMRSKYPDQDLMMEGKMS-YCTTGQMMHSS 242
QY 243 YQGIFELKENDRIPVSYTNEHLIDMDHEASFFGAF 278
DB 243 YLGAVFNLTSDHLVYVSELVNFESQTFPGLY 278
RESULT 15
TNF6_HUMAN STANDARD: PRT: 281 AA.
ID TNF6_HUMAN
AC P48023; Q9BZP9;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
   (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN Name=TNFRSF6; Synonyms=APTL1G1, FASL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
   lymphocytes."
RL J. Exp. Med. 181:71-77(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species
   specificity."
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Schaeuble C.E., Poehmann R., Philippen P., Eibel H.;
RL Submitted (JUN-1995) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95071350; PubMed=780502;
RA Mita E., Haysashi N., Ito S., Takehara T., Hijioka T., Kasehara A.,
RA Fusumoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
   infection."
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;

```

RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
 RT "Isolation and characterization of a new naturally occurring variant of
 RT human Fas ligand that is expressed only in membrane bound form.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [61]
 RA P. SEQUENCE FROM N.A.
 RP Wilkinson J.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RA P. SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Blood;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Gronow L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wengner L., Shellen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schelter C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA DiCicco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stedilton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tohiyuki S., Carinetti P., Prange C.,
 RA Rata S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kelleman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RA P. SEQUENCE OF 1-10 FROM N.A.
 RP TISSUE=Blood;
 RC Matsumura M., Nakanishi Y., Ohba Y.;
 RA Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RA CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
 RP MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827;
 RA Schneider P., Bodmer J.-U., Holler N., Matmann C., Souderi P.,
 RA Tserikh A., Peltesch M.C., Tschopp J.;
 RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
 RL J. Biol. Chem. 272:18827-18833(1997).
 RN [10]
 RA PROCESSING.
 RP MEDLINE=98087475; PubMed=9427603;
 RA Tanaka M., Itai T., Adachi M., Nagata S.;
 RT "Downregulation of Fas ligand by shedding.";
 RL Nat. Med. 4:31-36(1998).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6/DCR3
 CC modulates its effects.
 CC -1- SUBUNIT: Homotrimer (Probable).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. May be released
 CC into the extracellular fluid, probably by cleavage form the cell
 CC surface.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC Name=2;
 CC Name=2; IsoId=P48023-1; Sequence=Displayed;
 CC Name=2; IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing.
 CC -1- DISEASE: Defects in TNFRSF6 are a cause of autoimmune
 CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
 CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome

[illegible]

SEQ SEQUENCE 281 AA; 31485 MW; A8A6EB358246E9BB CRC64;

Query Match 12.6%; Score 186; DB 1; Length 281;

Best Local Similarity 22.1%; Pred. No. 4.9e-07;

Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

```

Oy 4 MEVGGPSLIGTCVLIVIFTVLLQSLCVAV--TYVYFTNELKQMDKYSKSGIACFLKE 60
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 71 LKRGHNSTG-LCLVMPFMVIALVGLGGMFQLEHLOKELAELERESTQKHTASLEK 129
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Oy 61 DDSYMDPNDEBSMNSPCWQVKWQLRQLVKRMILRTSEETISTVQEKQONISPLVREGPQ 120
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 130 QIGHSPPE-----KKELRKV----- 146
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Oy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSRSGHSFLSNLHNGELVIHKG 180
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 147 ---AHLT---GRSNRSMP-----LEWEDT-YGIVLLSGVKYKKGGLVINETG 187
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Oy 181 FYIYSQTYFRFOEIKENTKNDKQWQYIY-KYTSYPDPILLMKSAKNS-----CMGK 233
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 188 LYFVTSKYVFRQ-----SCNNLPISHKVIYRNSKYFODLVMEGKMMSYCTTGOMMAR 241
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Oy 234 DAHYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAP 278
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 242 -----SSYLGAVFNLTSADHLVYNVSELSLVNFEESQTFPGLY 279
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

```

Search completed: March 2, 2005, 14:50:42
Job time : 179 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 14:50:47 ; Search time 25 Seconds

(without alignments)
505.326 Million cell updates/sec

Title: US-10-077-435-1

Perfect score: 1478
Sequence: 1 MAMMEVGGPSLIGOTCVLIV.....NEHLIDMDHESFGAFPLVG 281

Scoring table:

BLOSUM62

Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 181127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:
1: /cgn2_6/ptodata/2/paa/BCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1478 | 100.0 | 281 | 6 | US-10-077-435-1 |
| 2 | 1478 | 100.0 | 281 | 7 | US-11-028-780-20 |
| 3 | 813 | 55.0 | 163 | 6 | US-10-839-694A-4 |
| 4 | 251.5 | 17.0 | 317 | 7 | US-11-028-780-22 |
| 5 | 230.5 | 15.6 | 170 | 5 | US-09-791-153E-157 |
| 6 | 228.5 | 15.5 | 155 | 6 | US-10-839-694A-6 |
| 7 | 186 | 12.6 | 281 | 7 | US-11-028-780-12 |
| 8 | 186 | 12.6 | 281 | 7 | US-11-054-539-6 |
| 9 | 166 | 11.2 | 251 | 7 | US-11-028-780-38 |
| 10 | 160 | 10.8 | 174 | 7 | US-11-028-780-36 |
| 11 | 159.5 | 10.8 | 240 | 7 | US-11-028-780-34 |
| 12 | 149.5 | 10.1 | 260 | 6 | US-10-916-286A-73 |
| 13 | 147.5 | 10.0 | 260 | 6 | US-10-916-286A-65 |
| 14 | 147.5 | 10.0 | 261 | 1 | PCT-US05-02350-136 |
| 15 | 147.5 | 10.0 | 261 | 7 | US-11-021-951-143 |
| 16 | 147.5 | 10.0 | 261 | 7 | US-11-028-780-10 |
| 17 | 147.5 | 10.0 | 261 | 7 | US-11-043-770-136 |
| 18 | 147.5 | 10.0 | 263 | 6 | US-10-450-763-52743 |
| 19 | 136.5 | 9.2 | 211 | 6 | US-10-916-286A-78 |
| 20 | 134.5 | 9.1 | 211 | 6 | US-10-916-286A-70 |
| 21 | 125.5 | 8.5 | 233 | 1 | PCT-US05-02350-1147 |
| 22 | 125.5 | 8.5 | 233 | 1 | PCT-US05-02350-1155 |
| 23 | 125.5 | 8.5 | 233 | 7 | US-11-028-780-4 |
| 24 | 125.5 | 8.5 | 233 | 7 | US-11-043-770-1147 |
| 25 | 125.5 | 8.5 | 233 | 7 | US-11-043-770-1155 |

| | | | | | | |
|----|-------|-----|-----|---|---------------------|-------------------|
| 26 | 125.5 | 8.5 | 233 | 7 | US-11-054-539-3 | Sequence 3, Appl. |
| 27 | 125.5 | 8.5 | 233 | 8 | US-60-643-337-4 | Sequence 4, Appl. |
| 28 | 122 | 8.3 | 144 | 6 | US-10-839-694A-3 | Sequence 3, Appl. |
| 29 | 122 | 8.3 | 205 | 7 | US-11-033-545-304 | Sequence 304, App |
| 30 | 122 | 8.3 | 205 | 7 | US-11-028-780-2 | Sequence 2, Appl. |
| 31 | 122 | 8.3 | 205 | 7 | US-11-054-539-4 | Sequence 4, Appl. |
| 32 | 122 | 8.3 | 217 | 1 | PCT-US05-02350-1146 | Sequence 1146, Ap |
| 33 | 122 | 8.3 | 217 | 7 | US-11-043-770-1146 | Sequence 1146, Ap |
| 34 | 122 | 8.3 | 251 | 7 | US-11-033-545-541 | Sequence 541, App |
| 35 | 119.5 | 8.1 | 240 | 7 | PCT-US05-02350-137 | Sequence 137, App |
| 36 | 119.5 | 8.1 | 240 | 7 | US-11-043-770-137 | Sequence 137, App |
| 37 | 118 | 8.0 | 240 | 1 | PCT-US05-02350-326 | Sequence 326, App |
| 38 | 118 | 8.0 | 240 | 7 | US-11-043-770-326 | Sequence 326, App |
| 39 | 117 | 7.9 | 146 | 6 | US-10-839-694A-5 | Sequence 5, Appl. |
| 40 | 117 | 7.9 | 152 | 6 | US-10-839-694A-2 | Sequence 2, Appl. |
| 41 | 116.5 | 7.9 | 157 | 5 | US-09-920-137C-9 | Sequence 9, Appl. |
| 42 | 116.5 | 7.9 | 157 | 5 | US-09-927-703A-1 | Sequence 1, Appl. |
| 43 | 116.5 | 7.9 | 157 | 6 | US-10-697-628B-9 | Sequence 9, Appl. |
| 44 | 116.5 | 7.9 | 157 | 6 | US-10-954-900A-9 | Sequence 9, Appl. |
| 45 | 116.5 | 7.9 | 157 | 7 | US-11-053-750-1 | Sequence 1, Appl. |

ALIGNMENTS

```
RESULT 1
US-10-077-435-1
; Sequence 1, Application US/10077435
; GENERAL INFORMATION:
; APPLICANT: Kumar, M. Vijay
; TITLE OF INVENTION: Treatment of Prostate Cancer
; FILE REFERENCE: M0351-268908
; CURRENT APPLICATION NUMBER: US/10/077,435
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,698
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-435-1

Query Match      100.0%; Score 1478; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 4.1e-129;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVGGPSLIGOTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYSKSGIACFLKE 60
DB      1 MAMMEVGGPSLIGOTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYSKSGIACFLKE 60
QY      61 DDSYVDPNDEBSMNSPCMQVVKQOLQVLRKMLRTSEETISTVDEKQONISPLVERGPQ 120
DB      61 DDSYVDPNDEBSMNSPCMQVVKQOLQVLRKMLRTSEETISTVDEKQONISPLVERGPQ 120
QY      121 RVAAHITTRGRSNTLSSPNSKNEKALCRKINSMESSSGHSFSLNHLRNGELVIHKG 180
DB      121 RVAAHITTRGRSNTLSSPNSKNEKALCRKINSMESSSGHSFSLNHLRNGELVIHKG 180
QY      181 FVYISQTYFPPFOEIKENTKNDKQOVYIKYKTSYPPPIILMSARNSCKDAEYGLY 240
DB      181 FVYISQTYFPPFOEIKENTKNDKQOVYIKYKTSYPPPIILMSARNSCKDAEYGLY 240
QY      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHESFGAFPLVG 281
DB      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHESFGAFPLVG 281

RESULT 2
US-11-028-780-20
; Sequence 20, Application US/11028780
; GENERAL INFORMATION:
```

```

/ APPLICANT: Human Genome Sciences, Inc.,
/ TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
/ FILE REFERENCE: PF559C1
/ CURRENT APPLICATION NUMBER: US/11/028,780
/ PRIOR FILING DATE: 2005-01-05
/ PRIOR APPLICATION NUMBER: 10/202,062
/ PRIOR FILING DATE: 2002-07-25
/ PRIOR APPLICATION NUMBER: 60/307,838
/ PRIOR FILING DATE: 2001-07-27
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 20
/ LENGTH: 281
/ TYPE: PRT
/ ORGANISM: human
US-11-028-780-20

Query Match      100.0%; Score 1478; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 4,1e-129;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTGVLIIVFTVLLQSLCAVATVYVYFNNELKQMDKYSKSGIACPLKE 60
DB 1 MAMMEVGGPSLGGTGVLIIVFTVLLQSLCAVATVYFNNELKQMDKYSKSGIACPLKE 60
QY 61 DDSYMDPNDESMNSPCQVQKQLRQVLRKMLRTSEETISTVQEKQONISPLVERGPO 120
DB 61 DDSYMDPNDESMNSPCQVQKQLRQVLRKMLRTSEETISTVQEKQONISPLVERGPO 120
QY 121 RYAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVTHE 180
DB 121 RYAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVTHE 180
QY 181 FYIYSQTYFRPQEEIKENTKNDKQVQYIYKTSYPPDILMKSRARNSCWSKDAEYGL 240
DB 181 FYIYSQTYFRPQEEIKENTKNDKQVQYIYKTSYPPDILMKSRARNSCWSKDAEYGL 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPFLVG 281

RESULT 3
US-10-839-694A-4
/ Sequence 4, Application US/10839694A
/ GENERAL INFORMATION:
/ APPLICANT: Li, Yuling
/ APPLICANT: Oren, Deena
/ APPLICANT: Arnold, Edward
/ APPLICANT: Volovik, Yulia
/ TITLE OF INVENTION: Crystalline Neutrokin-alpha Protein, Method of preparation
/ FILE REFERENCE: PF567
/ CURRENT APPLICATION NUMBER: US/10/839,694A
/ CURRENT FILING DATE: 2004-05-06
/ PRIOR APPLICATION NUMBER: PCT/US02/35661
/ PRIOR FILING DATE: 2002-11-07
/ PRIOR APPLICATION NUMBER: 60/331,049
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 4
/ LENGTH: 163
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (15)..(15)
/ OTHER INFORMATION: Xaa equals Ser; omitted at asterisk in TRAIL sequence depicted in
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (16)..(16)

```

```

/ OTHER INFORMATION: Xaa equals Asn; omitted at asterisk in TRAIL sequence depicted in
/ OTHER INFORMATION: Figure 1
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (17)..(17)
/ OTHER INFORMATION: Xaa equals Thr; omitted at asterisk in TRAIL sequence depicted in
/ OTHER INFORMATION: Figure 1
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (18)..(18)
/ OTHER INFORMATION: Xaa equals Leu; omitted at asterisk in TRAIL sequence depicted in
/ OTHER INFORMATION: Figure 1
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (19)..(19)
/ OTHER INFORMATION: Xaa equals Ser; omitted at asterisk in TRAIL sequence depicted in
/ OTHER INFORMATION: Figure 1
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (20)..(20)
/ OTHER INFORMATION: Xaa equals Pro; omitted at asterisk in TRAIL sequence depicted in
/ OTHER INFORMATION: Figure 1
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (21)..(21)
/ OTHER INFORMATION: Xaa equals Arg; omitted at asterisk in TRAIL sequence depicted in
/ OTHER INFORMATION: Figure 1
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (22)..(22)
/ OTHER INFORMATION: Xaa equals Asn; omitted at asterisk in TRAIL sequence depicted in
/ OTHER INFORMATION: Figure 1
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (23)..(23)
/ OTHER INFORMATION: Xaa equals Ser omitted at asterisk in TRAIL sequence depicted in
/ OTHER INFORMATION: Figure 1
US-10-839-694A-4

Query Match      55.0%; Score 813; DB 6; Length 163;
Best Local Similarity 94.5%; Pred. No. 6,2e-68;
Matches 154; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 119 PQRYAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVTHE 178
DB 1 PQRYAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVTHE 178
QY 179 KGFYIYSQTYFRPQEEIKENTKNDKQVQYIYKTSYPPDILMKSRARNSCWSKDAEYGL 238
DB 61 KGFYIYSQTYFRPQEEIKENTKNDKQVQYIYKTSYPPDILMKSRARNSCWSKDAEYGL 120
QY 239 LYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPFLVG 281
DB 121 LYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPFLVG 163

RESULT 4
US-11-028-780-22
/ Sequence 22, Application US/11028780
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.,
/ TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
/ FILE REFERENCE: PF559C1
/ CURRENT APPLICATION NUMBER: US/11/028,780
/ CURRENT FILING DATE: 2005-01-05
/ PRIOR APPLICATION NUMBER: 10/202,062
/ PRIOR FILING DATE: 2002-07-25
/ PRIOR APPLICATION NUMBER: 60/307,838
/ PRIOR FILING DATE: 2001-07-27
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 22
/ LENGTH: 317

```



```

; TYPE: PRT
; ORGANISM: human
US-11-028-780-22

Query Match      17.0%; Score 251.5; DB 7; Length 317;
Best Local Similarity 24.1%; Pred. No. 1.2e-15;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

QY 10 PSLGTCVLIVFTVLQSLCAVAVYVFTNELKQMDKXSGIACF-----LXKD----- 61
DB 42 PAAASHMFALLGLGLGQVAVFVFRQAQND--PNRISBDGTCYIRILRLHENDAF 99
QY 62 -DSYDNDPDEESMNSPCQVKN-----QLRQVAKKILRTSEETI-----STVOEKO 107
DB 100 QDTTLESQDTKILPDSCKRIKQAFQAVQKELQHVSGHIAEKAMVSGMIDLAKRSK 159
QY 108 QNISPLVBERGFORVAHAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167
DB 160 LEAQPF-----AHLT-----INATDIPSGSHKVSLSL---SSWYHDR-GMAKISNM 199

QY 168 HLRNDELVIHEKGFYIYISQTYFRPOEIKENTKNDKQVQIYKYT-SYDPDILMKSA 226
DB 200 TFSNKLIVNQDGFYLLVYLVANICFRHHTSGDLATEYLQLMVYVTKSIKIPSSHTLMKG 259
QY 227 RNSCKSKAEYGLYSIYQCGIFELKENDRIFVSVTNEHLIDMDHSAFPGAFV 280
DB 260 STKYSNGSEHFHYSINVGGFKLRSGERISIEVSNPSLDDPDATYFGAFKV 313

RESULT 5
US-09-791-153E-157
; Sequence 157, Application US/09791153E
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra V.
; APPLICANT: Hitz, Anne
; APPLICANT: Boyle, William J.
; APPLICANT: Sullivan, John K.
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153E
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 157
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153E-157

Query Match      15.6%; Score 230.5; DB 5; Length 170;
Best Local Similarity 34.2%; Pred. No. 4.6e-14;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY 124 AHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLRLNGELVIHEKGFY 183
DB 19 AHLT-----INAASTPSGSHKVTL---SSWYHDR-GMAKISMTLTSNGELRVNQDGFY 68
QY 184 IYSQTYFRPOEIKENTKNDKQVQIYKYT-SYDPDILMKSA RNSCKSKAEYGLYSI 242
DB 69 LVANICFRHHTSGDLATEYLQLMVYVTKSIKIPSSHMLMKGSTRKMSGNSSEHFHYSI 128
QY 243 YQGGIFELKENDRIFVSVTNEHLIDMDHSAFPGAFV 280
DB 129 NVGGFFKLRSGERISIEVSNPSLDDPDATYFGAFKV 166

RESULT 6
US-10-839-694A-6
; Sequence 6, Application US/10839694A
; GENERAL INFORMATION:
; APPLICANT: Li, Yuling
```

```

; APPLICANT: Oren, Deena
; APPLICANT: Arnold, Edward
; APPLICANT: Volovik, Yulia
; TITLE OF INVENTION: Crystalline Neutrokin-alpha Protein, Method of preparation
; FILE REFERENCE: PF567
; CURRENT APPLICATION NUMBER: US/10/839,694A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/US02/35661
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/331,049
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-839-694A-6

Query Match      15.5%; Score 228.5; DB 6; Length 155;
Best Local Similarity 34.2%; Pred. No. 6.3e-14;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY 124 AHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLRLNGELVIHEKGFY 183
DB 4 AHLT-----INAASTPSGSHKVTL---SSWYHDR-GMAKISMTLTSNGELRVNQDGFY 53
QY 184 IYSQTYFRPOEIKENTKNDKQVQIYKYT-SYDPDILMKSA RNSCKSKAEYGLYSI 242
DB 54 LVANICFRHHTSGVPTDYQLQLMVYVTKSIKIPSSHMLMKGSTRKMSGNSSEHFHYSI 113
QY 243 YQGGIFELKENDRIFVSVTNEHLIDMDHSAFPGAFV 280
DB 114 NVGGFFKLRSGERISIEVSNPSLDDPDATYFGAFKV 151

RESULT 7
US-11-028-780-12
; Sequence 12, Application US/11028780
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559C1
; CURRENT APPLICATION NUMBER: US/11/028,780
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 10/202,062
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-11-028-780-12

Query Match      12.6%; Score 186; DB 7; Length 281;
Best Local Similarity 22.1%; Pred. No. 1.1e-09;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

QY 4 MEVQGPSIGQTCVLIVFTVLQSLCAVAV---TYVFTNELKQMDKXSGIACFLKE 60
DB 71 LKKRGHSTG-LCLVMFPMVLVALVGLGNFOLHOKELAELESTQHTASSLEK 129
QY 61 DSYDNDPDEESMNSPCQVKNQLRQVAKKILRTSEETISTVOEKOQNISPLVBERGPO 120
DB 130 QIHPSPPPE-----KKELRKV----- 146
QY 121 RVAHAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLRLNGELVIHEKGFY 180
DB 147 ---AHLT---GKSNRSMP-----LEWEDT-YGIVLGQVKKYKGLVINYENG 187
```

[illegible]

RESULT 8
US-11-054-539-6

```

; TITLE OF INVENTION: Neutrokrine-alpha and Neutrokrine-alpha Splice Variant
;
; FILE REFERENCE: PF343P6
;
; CURRENT APPLICATION NUMBER: US/11/054,539
;
; COUNTRY OF ORIGIN: 0000 0000 00

```

```

1  CURRENT FILING DATE: 2005-02-10
2  PRIOR APPLICATION NUMBER: 60/543,261
3  PRIOR FILING DATE: 2004-02-11
4  PRIOR APPLICATION NUMBER: 60/580,387
5  PRIOR FILING DATE: 2004-06-18
6  PRIOR APPLICATION NUMBER: 60/617,131
7  PRIOR FILING DATE: 2004-10-12
8  PRIOR APPLICATION NUMBER: 10/739,042
9  PRIOR FILING DATE: 2003-12-19
10 PRIOR APPLICATION NUMBER: 10/735,865
11 PRIOR FILING DATE: 2003-12-16
12 PRIOR APPLICATION NUMBER: 10/270,487
13 PRIOR FILING DATE: 2002-10-16
14 PRIOR APPLICATION NUMBER: 60/366,548
15 PRIOR FILING DATE: 2002-04-01
16 PRIOR APPLICATION NUMBER: 60/336,726
17 PRIOR FILING DATE: 2001-12-07
18 PRIOR APPLICATION NUMBER: 60/331,478
19 PRIOR FILING DATE: 2001-11-16
20 PRIOR APPLICATION NUMBER: 60/330,835
21 PRIOR FILING DATE: 2001-10-31
22 Remaining Prior Application data removed - See File Wrapper or PALM
23 NUMBER OF SEQ ID NOS: 59

```

```

; SEQ ID NO 6
; LENGTH: 281
; TYPE: prt
; ORGANISM: Homo sapiens
; US-11-054-539-6

```

Query Match 12.6%; Score 186; DB 7; Length 281;
Best Local Similarity 22.1%; Pred. NO. 1.1e-09;
Matches 63; Conservative 82; Indels 86; Gaps 11

[illegible]

```
OY      121 RVAAHITGTGRSNTLSSPNSKNEKALGKRINSWESSRSGHFLSNLHLRNGLVIHEKG 180Q
        ||:||:|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      147 ---AHLT---CKSNSRSM-----LEMEDT-YGIVLISGVYKKGGIVINETG 187
```

```
QY      181 FYYIYSQTYPFRFOEIKENTKNDKWQVLY- KTSISPDPILMKSRNS-----CWSK 233
          |::||| | : : : || ::|
Db      188 LYFVYSKVYRFG-----SCNNLPISHKYVRANSKTPQDLVMMEGKNMSYCTTGOMMAR 241
```

```

QY      234 DAETGLSYIGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAF 278
          | | | | | | | | | | | | | | | | | | | | | |
Db      242 -----SSYLGAVFNLTSADHLVYVNSELSLVNFEESQTFGLY 279

```

RESULT 9

```

US-11-028-780-38
; Sequence 38, Application US/11028780
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PP559C1
; CURRENT APPLICATION NUMBER: US/11/028,780
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 10/0202,062
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 251
; TYPE: prt
; ORGANISM: human
US-11-028-780-38

```

| Query Match | 1.1.28; Score 166; DB 7; Length 251; |
|-------------|--------------------------------------|
| | |

Best Local Similarity 33.2%; Pred. No. 6.9e-08;
Matches 62; Conservative 30; Mismatches 65; Indels 30; Gaps 12

QY 107 QQNTSPVLRERGPQVAAHITGTGRSNTLSPNSK:-KALGRKINSWSSRSRGHFLS 165
 Db 82 QQVAPLRADGDKER--AHLTVA---QTPTQHKKNQPPAL-----HWE HELGLAFTK 129

Qy 166 N-LHLRRLGVHKEGFYIYSQVYFRFQ----SEIKENTKNDK--QMVOYIKYT-SYP 217
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 NRMYTYNKKLLIPESGDYFIITYSQVTRFGMTSECSEIRQAQRPNKDSDITVIATKYTDSYF 189

Qy 218 DPILMLKSRNRSCSKDAEYG---LYSIRGGIRELKKENDRIPASVTNEHILDMHE-AS 273
Db 190 EPTQLIMGKTSVC-----EVGSNNFQPIILGAMTSLSQEGKLMNVNSDISLVDTKEDKT 244

| | | | |
|----|-----|---------|-----|
| QY | 274 | FFGAFLV | 280 |
| | | : | |
| Db | 245 | FFGAFLV | 251 |

RESULT 1C
US-11-028

```

; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: P559c1
; CURRENT APPLICATION NUMBER: US/11/028,780

```

```

1  PRIOR APPLICATION NUMBER: 10/202,062
2  PRIOR FILING DATE: 2002-07-25
3  PRIOR APPLICATION NUMBER: 60/307,838
4  PRIOR FILING DATE: 2001-07-27
5  NUMBER OF SEQ ID NOS: 42
6  SOFTWARE: PatentIn version 3.2

```

```

; SEQ ID NO 36
; LENGTH: 174
; TYPE: PRT
; ORGANISM: human
US-11-028-780-36

```

| Query Match | 10.8% | Score 160 | DB 7 | Length 174 |
|-------------|-------|-----------|------|------------|
|-------------|-------|-----------|------|------------|

Best Local Similarity 35.3%; Pred. No. 1.6e-07;
Matches 49; Conservative 24; Mismatches 48; Indels 18; Gaps 8

QY 154 WESRRSGHFLSN-LIHRNGELVTHKEGFIYIYSTQYFEQ----EIKENTKNDK-QM 206

Db 42 WE-HELGLAFTKKNMNYTNKFKLLIPESGDYFIYSQVTFRMTSECEIRQGRPNKPSDI 100

QY 207 VQYLYKYT--SYDPDILLKMSARNSQWSKDAEYG---LVS1YQGGGFELKENDRIEVSVTN 262

Db 101 TVVTLTKVDSYEPETQLMGTKSVC-----EVGSNWFPQIPLYLGAHFSLQSGDCKLMVNSD 155

Qy 263 EHLIDMDHE-ASFGAFIV 280
Db 156 ISLVDTKEDKTFGAFEL 174

RESULT 11

US-11-028-780-34
Sequence 34, Application US/11028780
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.,
TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
FILE REFERENCE: PF559C1
CURRENT APPLICATION NUMBER: US/11/028,780
PRIOR FILING DATE: 2005-01-05
PRIOR APPLICATION NUMBER: 10/202,062
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34
LENGTH: 240
TYPE: PRT
ORGANISM: human
US-11-028-780-34

Query Match 10.8%; Score 159.5; DB 7; Length 240;
Best Local Similarity 23.8%; Pred. No. 2.6e-07;
Matches 53; Conservative 41; Mismatches 66; Indels 63; Gaps 9;

Qy 79 QYKWLQRLVRLKMLRTSEETSTVQEKQON-ISPVRERGQVRAHITGRGENTLIS 137
Db 60 QHMRGKGVNLTLPDGPAGSMEOQLQERSHEVNP-----AAHLTGANSSLTGSG 109
Qy 138 SPNSKNEKALGRKINSMESSRSQHSPLSNLHNLNGELVHEKGFYIYSQTYFRFOEBIK 197
Db 110 GP-----LIME-TQGLAFRLRGLSYHDGLVLTQKGYIYISK----- 146
Qy 198 ENTQDKQNVQY-----YKKT-STPDPILMLKSKARNSCWSDAEYGLY 240
Db 147 -----VOLGVCPLGLASTITNGLYKTRPYRPELELIVSQSPCGRATSSRYV 197
Qy 241 --SIYGGIFELKENDRIFVSVTNEHLIDM-DHEASFGAFIV 280
Db 198 WDSFUGVYVHLAGEEVRVLDKRLVRLDGTNSYFGAFIV 240

RESULT 12

US-10-916-286A-73
Sequence 73, Application US/10916286A
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
FILE REFERENCE: Drelitz, Matthew J.
TITLE OF INVENTION: CANINE IL-4 IMMUNOREGULATORY PROTEINS AND USES THEREOF
FILE REFERENCE: IM-2-CI-R
CURRENT APPLICATION NUMBER: US/10/916,286A
PRIOR FILING DATE: 2004-08-11
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 260
TYPE: PRT
ORGANISM: Felis catus
US-10-916-286A-73

Query Match 10.1%; Score 149.5; DB 6; Length 260;
Best Local Similarity 24.4%; Pred. No. 2.4e-06;
Matches 69; Conservative 57; Mismatches 114; Indels 43; Gaps 15;

Qy 2 AMMEVQGPSLQGTCLVLIPTVLL--QSLCAVATVYVFTNEIKQWQDKYSKGIACFLK 59
Db 9 APRSVATGPPVSMK-IFWYLVLTFLITQMGISALPAVYIHRLDKIEDERNLYEDVFMK 67
Qy 60 EDDSYWDPNDEESMNS--PCWQVQWLQRLVRLKMLRTSEETSTVQEKQONISPLVRR 117
Db 68 ---TLQCKNKGEGALSLNCEIEKSRFEAFLEIML--NKEF-----KKEKVA--MOK 114
Qy 118 GPQ--RVAAHITGTGRNSTLSSPNSKNEKALGRKINSMESSRSQHSPLSNL-HLNG-E 173
Db 115 GQDDPRVAHV-----ISEASSSTASVL-----QW-ARKGYTTISSNLVTLNKGQ 159
Qy 174 LVIEHKGFFYIYSQTYFRFOEBIKENTKNDKQWQVYIYKTSYPPDILMLKSKARNSCWSK 233
Db 160 LAVKQGLYIYAQVTFCSNR-----ASSQAFVSLCHSHSGSERVLRLAARNSSSK 215
Qy 234 DAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFG 276
Db 216 PC--GQOSIHLGVSFELHPGASVFNVTDPQVSHGTGFTSPG 256

RESULT 13

US-10-916-286A-65
Sequence 65, Application US/10916286A
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
FILE REFERENCE: Drelitz, Matthew J.
TITLE OF INVENTION: CANINE IL-4 IMMUNOREGULATORY PROTEINS AND USES THEREOF
FILE REFERENCE: IM-2-CI-R
CURRENT APPLICATION NUMBER: US/10/916,286A
PRIOR FILING DATE: 2004-08-11
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 65
LENGTH: 260
TYPE: PRT
ORGANISM: Canis familiaris
US-10-916-286A-65

Query Match 10.0%; Score 147.5; DB 6; Length 260;
Best Local Similarity 24.0%; Pred. No. 3.7e-06;
Matches 68; Conservative 55; Mismatches 117; Indels 43; Gaps 14;

Qy 2 AMMEVQGPSLQGTCLVLIPTVLL--QSLCAVATVYVFTNEIKQWQDKYSKGIACFLK 59
Db 9 APRSVATGPPVSMK-IFWYLVLTFLITQMGISALPAVYIHRLDKIEDERNLYEDVFMK 67
Qy 60 EDDSYWDPNDEESMNS--PCWQVQWLQRLVRLKMLRTSEETSTVQEKQONISPLVRR 117
Db 68 ---TLQCKNKGEGALSLNCEIEKSRFEAFLEIMLNE-----MKKEENIA--MOK 114
Qy 118 GPQ--RVAAHITGTGRNSTLSSPNSKNEKALGRKINSMESSRSQHSPLSNL-HLNG-E 173
Db 115 GQDDPRVAHV-----SEASSNPAS-----VLRN-ARKGYTTISSNLVTLNKGQ 159
Qy 174 LVIEHKGFFYIYSQTYFRFOEBIKENTKNDKQWQVYIYKTSYPPDILMLKSKARNSCWSK 233
Db 160 LAVKQGLYIYAQVTFCSNR-----ASSQAFVSLCHSHSGSERVLRLAARNSSSK 215
Qy 234 DAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFG 276
Db 216 PC--GQOSIHLGVSFELHPGASVFNVTDPQVSHGTGFTSPG 256

RESULT 14

PCT-US05-02350-136
Sequence 136, Application PC/TUS0502350
GENERAL INFORMATION:

```
/ APPLICANT: Ayalon-Soffer, Michael
/ APPLICANT: Levine, Zurit
/ APPLICANT: Sella-Tavor, Osnat
/ APPLICANT: Diber, Alex
/ APPLICANT: Shemesh, Ronen
/ APPLICANT: Toporik, Amir
/ APPLICANT: Rotman, Galit
/ APPLICANT: Nemzer, Sergey
/ APPLICANT: Rosenberg, Avi
/ APPLICANT: Dahary, Dvir
/ APPLICANT: Wool, Assaf
/ APPLICANT: Cojocaru, Gad S.
/ APPLICANT: Akiya, Pinchas
/ APPLICANT: Pollock, Sarah
/ APPLICANT: Savitsky, Klmaret
/ APPLICANT: Bernstein, Jeanne
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING
/ TITLE OF INVENTION: SAME
/ FILE REFERENCE: 28487
/ CURRENT APPLICATION NUMBER: PCT/US05/02350
/ CURRENT FILING DATE: 2005-02-10
/ NUMBER OF SEQ ID NOS: 1155
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 136
/ LENGTH: 261
/ TYPE: PRT
/ ORGANISM: Homo sapiens
PCT-US05-02350-136
```

```
Query Match 10.0%; Score 147.5; DB 1; Length 261;
Best Local Similarity 23.7%; Pred. No. 3.7e-06;
```

```
Matches 66; Conservative 51; Mismatches 99; Indels 63; Gaps 15;
```

```
QY 17 VLVIFVTLL--QSLCAVTYYFTNELKQMODKYSKGIACFLKEDDSYMDP-----ND 69
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 23 IFMYLLTVFLITQMGSLFAVYLHRRLDKIEDERN-----LHEDFVFMKTIORCNTG 75
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 EESNM-SPQWQVQWQLRQLVKMLRTSEETISTVQEQOONISPLVBERGPORVAHNTG 128
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 76 ERSLSLNCBEIKSQPEGFVDIML-NKET-----KENSPEMOKGDQNPQ-IAAHV-- 126
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 TGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSN--LHLRNG-ELVIEHKGYYIY 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 127 -----ISEASSKTTSVL-----QW--AEKGYTMSNNLVLENGKQLTVKRGGLYYIY 172
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 SQTFRFOBEIKENT-----KNDKQWQYIYKTTSTPDPILMKSRNSCWSKDAEY 237
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 173 AQVTFCSNREASSQAPFIASLCLKSPGRFR-----ILIRANTHSSAKPC-- 218
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 238 GLYSIYQGIPELKENDRIFVSVTNEHLIDMDHEASFFG 276
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 219 GQOSIHLGSGVFELQPGASVFVAVTDPDPSQVSHGTGFTSFG 257
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 15
US-11-021-951-143

/ Sequence 143, Application US/11021951

```
/ GENERAL INFORMATION:
/ APPLICANT: HAUPTS, Ulrich
/ APPLICANT: KOLTERMANN, Andre
/ APPLICANT: SCHEIDIG, Andreas
/ APPLICANT: VOTSMEIER, Christian
/ APPLICANT: Ketting, Ulrich
/ APPLICANT: COCO, Wayne Michael
/ TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
/ FILE REFERENCE: 04156.0002U5
/ CURRENT APPLICATION NUMBER: US/11/021,951
/ CURRENT FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: 10/872,198
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 60/543,518
/ PRIOR FILING DATE: 2004-02-11
```

```
/ PRIOR APPLICATION NUMBER: 60/524,960
/ PRIOR FILING DATE: 2003-11-25
/ PRIOR APPLICATION NUMBER: EP 04003058
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: EP 03025871
/ PRIOR FILING DATE: 2003-11-11
/ PRIOR APPLICATION NUMBER: EP 03025851
/ PRIOR FILING DATE: 2003-11-10
/ PRIOR APPLICATION NUMBER: EP 03013819
/ PRIOR FILING DATE: 2003-06-18
/ NUMBER OF SEQ ID NOS: 191
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 143
/ LENGTH: 261
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-021-951-143
```

```
Query Match 10.0%; Score 147.5; DB 7; Length 261;
```

```
Best Local Similarity 23.7%; Pred. No. 3.7e-06;
```

```
Matches 66; Conservative 51; Mismatches 99; Indels 63; Gaps 15;
```

```
QY 17 VLVIFVTLL--QSLCAVTYYFTNELKQMODKYSKGIACFLKEDDSYMDP-----ND 69
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 23 IFMYLLTVFLITQMGSLFAVYLHRRLDKIEDERN-----LHEDFVFMKTIORCNTG 75
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 EESNM-SPQWQVQWQLRQLVKMLRTSEETISTVQEQOONISPLVBERGPORVAHNTG 128
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 76 ERSLSLNCBEIKSQPEGFVDIML-NKET-----KENSPEMOKGDQNPQ-IAAHV-- 126
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 TGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSN--LHLRNG-ELVIEHKGYYIY 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 127 -----ISEASSKTTSVL-----QW--AEKGYTMSNNLVLENGKQLTVKRGGLYYIY 172
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 SQTFRFOBEIKENT-----KNDKQWQYIYKTTSTPDPILMKSRNSCWSKDAEY 237
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 173 AQVTFCSNREASSQAPFIASLCLKSPGRFR-----ILIRANTHSSAKPC-- 218
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 238 GLYSIYQGIPELKENDRIFVSVTNEHLIDMDHEASFFG 276
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 219 GQOSIHLGSGVFELQPGASVFVAVTDPDPSQVSHGTGFTSFG 257
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: March 2, 2005, 15:03:38
Job time : 26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 14:28:14 ; Search time 173 Seconds
(without alignments)
628.206 Million cell updates/sec

Title: US-10-077-435-1
Perfect score: 1478
Sequence: 1 MAMMEVGGPSLIGQTCVLIV.....NEHLIDMDHSAFCAPLWG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 1478 | 100.0 | 281 | AAW19777 | AAW19777 Novel cyt |
| 2 | 1478 | 100.0 | 281 | AAW27134 | AAW27134 Human Apo |
| 3 | 1478 | 100.0 | 281 | AAW19787 | AAW19787 Human Apo |
| 4 | 1478 | 100.0 | 281 | AAW76829 | AAW76829 Human TL2 |
| 5 | 1478 | 100.0 | 281 | AAW56760 | AAW56760 Human TRA |
| 6 | 1478 | 100.0 | 281 | AAW44354 | AAW44354 Human AGP |
| 7 | 1478 | 100.0 | 281 | AAW01517 | AAW01517 Protein a |
| 8 | 1478 | 100.0 | 281 | AAW27012 | AAW27012 Human Apo |
| 9 | 1478 | 100.0 | 281 | AAW81956 | AAW81956 Human Apo |
| 10 | 1478 | 100.0 | 281 | AAW24038 | AAW24038 Human PRO |
| 11 | 1478 | 100.0 | 281 | AAW08545 | AAW08545 Amino aci |
| 12 | 1478 | 100.0 | 281 | AAW28691 | AAW28691 Human AGP |
| 13 | 1478 | 100.0 | 281 | AAW50977 | AAW50977 Human PRO |
| 14 | 1478 | 100.0 | 281 | AAW67243 | AAW67243 Human Apo |
| 15 | 1478 | 100.0 | 281 | AAW11031 | AAW11031 Human TNF |
| 16 | 1478 | 100.0 | 281 | AAW48350 | AAW48350 Human TL2 |
| 17 | 1478 | 100.0 | 281 | AAW08133 | AAW08133 Human TRA |
| 18 | 1478 | 100.0 | 281 | AAW31630 | AAW31630 Human TRA |
| 19 | 1478 | 100.0 | 281 | AAW75062 | AAW75062 Human TNF |
| 20 | 1478 | 100.0 | 281 | AAW51077 | AAW51077 Human Apo |
| 21 | 1478 | 100.0 | 281 | AAW51954 | AAW51954 Human Apo |
| 22 | 1478 | 100.0 | 281 | AAW19095 | AAW19095 C neoforn |
| 23 | 1478 | 100.0 | 281 | AAW79593 | AAW79593 Human TNF |
| 24 | 1478 | 100.0 | 281 | AAW73861 | AAW73861 Human Apo |
| 25 | 1478 | 100.0 | 281 | AAW10205 | AAW10205 Human Apo |

| | | | | | |
|----|------|-------|-----|----------|--------------------|
| 26 | 1478 | 100.0 | 281 | ABU71443 | ABU71443 Human neo |
| 27 | 1478 | 100.0 | 281 | ABG72738 | ABG72738 Human TNF |
| 28 | 1478 | 100.0 | 281 | AAO29543 | AAO29543 Human TRA |
| 29 | 1478 | 100.0 | 281 | ABU08558 | ABU08558 Human TNF |
| 30 | 1478 | 100.0 | 281 | ABR42313 | ABR42313 Human TRA |
| 31 | 1478 | 100.0 | 281 | ABG71905 | ABG71905 Human TRA |
| 32 | 1478 | 100.0 | 281 | AAE36258 | AAE36258 Human TNF |
| 33 | 1478 | 100.0 | 281 | AAE36258 | AAE36258 Human TNF |
| 34 | 1478 | 100.0 | 281 | AAO31151 | AAO31151 Human TNF |
| 35 | 1478 | 100.0 | 281 | ABO25125 | ABO25125 Human TNF |
| 36 | 1478 | 100.0 | 281 | ADB61471 | ADB61471 Native hu |
| 37 | 1478 | 100.0 | 281 | ADC35202 | ADC35202 Human TNF |
| 38 | 1478 | 100.0 | 281 | ADD14080 | ADD14080 Human TRC |
| 39 | 1478 | 100.0 | 281 | ADD19010 | ADD19010 Human TRC |
| 40 | 1478 | 100.0 | 281 | ABW02276 | ABW02276 Human TRA |
| 41 | 1478 | 100.0 | 281 | ADE76953 | ADE76953 Human pro |
| 42 | 1478 | 100.0 | 281 | ADK72311 | ADK72311 Human Apo |
| 43 | 1478 | 100.0 | 281 | ADK72303 | ADK72303 Human Apo |
| 44 | 1478 | 100.0 | 281 | ADK72304 | ADK72304 Human Apo |
| 45 | 1478 | 100.0 | 281 | ADK72296 | ADK72296 Human w11 |

ALIGNMENTS

| | | |
|----------|--|---|
| RESULT 1 | AAW19777 | standard; protein; 281 AA. |
| ID | AAW19777 | |
| XX | AAW19777; | |
| AC | AAW19777; | |
| XX | | |
| DT | 22-SBP-1997 (first entry) | |
| XX | | |
| DE | Novel cytokine Apo-2 ligand. | |
| XX | | |
| KW | Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PH | Key | Location/Qualifiers |
| FT | Peptide | 1..281 |
| FT | | /note= "Claim 4" |
| FT | Region | 1..14 |
| FT | | /label= Cytoplasmic_region |
| FT | Protein | 15..281 |
| FT | | /note= "Claim 3" |
| FT | Region | 15..40 |
| FT | | /label= Transmembrane_region |
| FT | Protein | 41..281 |
| FT | | /note= "Claim 2" |
| FT | Region | 41..281 |
| FT | | /label= Extracellular_region |
| FT | Modified-site | 109 |
| FT | | /label= Glycosylation |
| FT | Protein | /note= "putative N-linked glycosylation site" |
| FT | | 114..281 |
| FT | | /note= "Claim 1" |
| XX | | |
| XX | WO9725428-A1. | |
| XX | | |
| XX | 17-JUL-1997. | |
| XX | | |
| XX | 08-JAN-1997; | 97WO-US000272. |
| XX | | |
| XX | 09-JAN-1996; | 96US-00584031. |
| XX | | |
| XX | (GETH) GENENTECH INC. | |
| XX | Ashkenazi AJ, Chuncharapal A, Kim KJ; | |
| XX | | |
| XX | WPI: 1997-372867/34. | |
| XX | | |
| XX | N-PSDB; AAT72796. | |

PT Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
PT apoptosis for the treatment of breast and colon cancer.

PS Claim 4; Fig 1a; 72pp; English.

XX A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian
CC cell apoptosis. It is believed to be a member of the tumour necrosis
CC factor cytokine family. Its amino acid sequence was deduced from a cDNA
CC clone (AAT72796) isolated from a human placental cDNA library. Apo-2
CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
CC transformed or transfected with a vector contg. Apo-2 ligand nucleic
CC acid. They can be used to induce apoptosis in mammals and to treat
CC pathological conditions such as cancer (esp. breast or colon cancer) or
CC to raise antibodies useful in diagnostic assays

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVIFTVLQSLCAVATVYVFTNELKQMDKYSKSGIACPLKE 60
DB 1 MAMMEVGGPSLGGTCVLIVIFTVLQSLCAVATVYVFTNELKQMDKYSKSGIACPLKE 60
QY 61 DSYNDPNDDESMNSPCQVQKQOLRVKRMILRTSEETISTVQKQONISPLVERGQ 120
DB 61 DSYNDPNDDESMNSPCQVQKQOLRVKRMILRTSEETISTVQKQONISPLVERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
QY 181 FYYIYSQTYFRPQOEIKENTKNDKQVQIYKYTSPDPILMLKSARNSCSKDAEYGLY 240
DB 181 FYYIYSQTYFRPQOEIKENTKNDKQVQIYKYTSPDPILMLKSARNSCSKDAEYGLY 240
QY 241 STYGGIFELKENDRIFFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 STYGGIFELKENDRIFFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 2
AAW27134
ID AAW27134 standard; protein; 281 AA.

AC AAW27134;

DT 02-APR-1998 (first entry)

XX Human Apoptosis inducing molecule-I (AIM-I).

XX Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
XX tumour necrosis factor ligand superfamily; AIM-I altered expression;
KW neoplasia inhibition; anti-inflammatory agent.

XX Homo sapiens.

OS Homo sapiens.

PN WO9733899-A1.

PD 18-SEP-1997.

PF 14-MAR-1996; 96WO-US003773.

PR 14-MAR-1996; 96WO-US003773.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM;

XX WPI; 1997-470807/43.

DR N-PSDB; AAT85210.

XX New Isolated apoptosis inducing molecule-I - used to develop products for
PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
PT versus host disease or inflammation.

PS Claim 2; Fig 1; 82pp; English.

XX The present sequence represents a human Apoptosis inducing molecule-I
XX (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
XX superfamily. The products can be used in the diagnosis and treatment of
XX disorders related to under-expression, over-expression or altered
XX expression of AIM-I. AIM-I or agonists can be used for treating
XX autoimmune disorders including systemic lupus erythematosus,
XX angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
XX diabetes, and multiple sclerosis, graft versus host disease, to inhibit
XX neoplasia such as tumour cell growth, to treat restenosis, to regulate
XX haematopoiesis in endothelial cell development, to stimulate peripheral
XX tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
XX used for treating cachexia, cerebral malaria, rheumatoid arthritis or
XX osteoporosis, for preventing graft-host rejection, and as anti-
XX inflammatory agents, for treating endotoxin shock or to prevent
XX activation of HIV

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVIFTVLQSLCAVATVYVFTNELKQMDKYSKSGIACPLKE 60
DB 1 MAMMEVGGPSLGGTCVLIVIFTVLQSLCAVATVYVFTNELKQMDKYSKSGIACPLKE 60
QY 61 DSYNDPNDDESMNSPCQVQKQOLRVKRMILRTSEETISTVQKQONISPLVERGQ 120
DB 61 DSYNDPNDDESMNSPCQVQKQOLRVKRMILRTSEETISTVQKQONISPLVERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
QY 181 FYYIYSQTYFRPQOEIKENTKNDKQVQIYKYTSPDPILMLKSARNSCSKDAEYGLY 240
DB 181 FYYIYSQTYFRPQOEIKENTKNDKQVQIYKYTSPDPILMLKSARNSCSKDAEYGLY 240
QY 241 STYGGIFELKENDRIFFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 STYGGIFELKENDRIFFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 3
AAW19787
ID AAW19787 standard; protein; 281 AA.

AC AAW19787;

DT 24-SEP-1997 (first entry)

XX Human apoptosis inducer cytokine TRAIL.

XX Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
KW thrombotic microangioplasty; therapy.

XX Homo sapiens.

OS Homo sapiens.

PN WO9733899-A1.

PD 18-SEP-1997.

PF 14-MAR-1996; 96WO-US003773.

PR 14-MAR-1996; 96WO-US003773.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM;

XX WPI; 1997-470807/43.

DR N-PSDB; AAT85210.

FT FT /label= Extracellular domain
FT FT /note= "contains a receptor-binding region"
FT FT 89..90
FT Cleavage-site
FT /note= "potential KEX2 protease processing site"
FT Modified-site
FT 109..111
FT /note= "potential N-glycosylation site"
FT Cleavage-site
FT 149..150
FT /note= "potential KEX2 protease processing site"
XX MO9701633-A1.
XX
XX
XX 16-JAN-1997.
XX PD
XX PF 25-JUN-1996; 96WO-US010895.
XX PR 29-JUN-1995; 95US-00496632.
XX PR 01-NOV-1995; 95US-00548368.
XX (IMMUNEX) IMMUNEX CORP.
XX PA
XX PI Wiley SR, Goodwin RG;
XX DR WPI, 1997-118715/11.
XX DR N-PSDB; AAT72847.
XX
XX TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
PT cells - useful for treating thrombotic microangiopathy, cancer and viral
PT infection and for use in assays.
XX
XX Claim 10; Page 43-44; 62pp; English.
XX
XX Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
CC (AAW19787) is a novel cytokine that induces apoptosis of certain target
CC cells, including cancer cells and virally infected cells. Its amino acid
CC sequence was deduced from cDNA clone Hualc (AAT72848), deposited in
CC vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
CC polypeptides) can be expressed in host cells and used in the treatment of
CC cancer (e.g. leukemia, lymphoma and melanoma) and viral infections, or
CC to raise antibodies that may be useful for treating thrombotic
CC microangiopathies
CC
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137; Indels 0; Gaps 0;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVOGSPSLGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVOGSPSLGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYDNDPNDDESNMSPCQWQKQOLVVRKMLRTSEETISTVQEQKQINISPLVBERGQ 120
DB 61 DDSYDNDPNDDESNMSPCQWQKQOLVVRKMLRTSEETISTVQEQKQINISPLVBERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGLVYHENG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGLVYHENG 180
QY 181 FYIYSQTYFRFOEIKENTKDKOMVOYIYKTYSPDPILLMKSRNSCWDAYEGLY 240
DB 181 FYIYSQTYFRFOEIKENTKDKOMVOYIYKTYSPDPILLMKSRNSCWDAYEGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
RESULT 4
AAW76829
ID AAW76829 standard; protein; 281 AA.
XX
AC AAW76829;

XX XX
XX 25-JAN-1999 (first entry)
XX
XX Human TNF2 protein.
XX
XX TR6; tumour necrosis factor related receptor; human; treatment; stroke;
XX inflammation; arthritis; septicemia; autoimmune disease; restenosis;
XX transplant rejection; infection; ischemia; brain injury; bone disease;
XX acute respiratory disease syndrome; acquired autoimmune disease syndrome;
XX AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;
XX TNF2. tumour necrosis factor-related apoptosis-inducing ligand.
XX
XX Homo sapiens.
XX
XX EP870827-A2.
XX
XX 14-OCT-1998.
XX PD
XX PF 23-DEC-1997; 97EP-00310562.
XX
XX 14-MAR-1997; 97US-0041230P.
XX PR 09-MAY-1997; 97US-00853684.
XX PR 22-AUG-1997; 97US-00916625.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Deen KC, Young PR;
XX
XX WPI, 1998-523156/45.
XX DR N-PSDB; AAV63096.
XX
XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding
PT polypeptide, antibody, agonist, antagonist, etc.
XX
XX Disclosure; Page 32-33; 34pp; English.
XX
XX This sequence represents the human tumour necrosis factor (TNF)-related
CC receptor, TNF2 (also known as tumour necrosis factor-related apoptosis-
CC inducing ligand, TRAIL). This protein is used in a method resulting in
CC the isolation of the novel human TNF related receptor, TR6. TR6
CC polypeptides and polynucleotides can be used in the treatment of chronic
CC and acute inflammation, arthritis, septicemia, autoimmune diseases (e.g.
CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
CC host disease, infection, stroke, ischemia, acute respiratory disease
CC syndrome, restenosis, brain injury, (acquired autoimmune disease
CC syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative
CC disorders), atherosclerosis and Alzheimers disease
CC
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137; Indels 0; Gaps 0;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVOGSPSLGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVOGSPSLGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYDNDPNDDESNMSPCQWQKQOLVVRKMLRTSEETISTVQEQKQINISPLVBERGQ 120
DB 61 DDSYDNDPNDDESNMSPCQWQKQOLVVRKMLRTSEETISTVQEQKQINISPLVBERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGLVYHENG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGLVYHENG 180
QY 181 FYIYSQTYFRFOEIKENTKDKOMVOYIYKTYSPDPILLMKSRNSCWDAYEGLY 240
DB 181 FYIYSQTYFRFOEIKENTKDKOMVOYIYKTYSPDPILLMKSRNSCWDAYEGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

```

RESULT 5
AAW56760
ID AAW56760 standard; protein; 281 AA.
XX
XX AAW56760;
AC
XX
XX 05-AUG-1998 (first entry)
DT
XX
XX Human TRAIL polypeptide.
DE
XX
XX Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
KW cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 1..18
FT /note= "N-terminal cytoplasmic domain"
FT Region 19..38
FT /note= "transmembrane region"
FT Domain 39..281
FT /note= "extracellular domain"
XX
XX US5763223-A.
PN
XX 09-JUN-1998.
PD
XX
XX 25-JUN-1996; 96US-00670354.
PF
XX 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548368.
XX
XX (IMMV ) IMMUNEX CORP.
PA
XX Goodwin RG, Wiley SR;
PI
XX WPI; 1998-347322/30.
DR N-PSDB; AAV29518.
XX
XX DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
PT for producing recombinant polypeptides for research and therapy of
PT leukaemia, lymphoma, melanoma and viral infections.
XX
XX Claim 1; Col 33-36; 28pp; English.
XX
XX This represents a human tumour necrosis factor related apoptosis ligand
CC (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
CC apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful
CC for producing the recombinant TRAIL polypeptides, which may be useful in
CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
CC (e.g. to isolate antigens for vaccine development). The polypeptides can
CC be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
CC treatment of blood or bone-marrow), or to treat viral infections
CC
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGSPSLGQTCVLIVFTVLLQSLCAVATVYVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGSPSLGQTCVLIVFTVLLQSLCAVATVYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYDNDPNDSESMNSPCWQVQKQOLVAKMILRTSEETISTVQEKQNIISPLVBERGQ 120
DB 61 DDSYDNDPNDSESMNSPCWQVQKQOLVAKMILRTSEETISTVQEKQNIISPLVBERGQ 120
QY 121 RVAAHITGRRGSRNTLSSPNSKNEKALGKINSWESSRSGHSFLSYHLRNELVYHEHG 180
DB 121 RVAAHITGRRGSRNTLSSPNSKNEKALGKINSWESSRSGHSFLSYHLRNELVYHEHG 180

```

```

QY 181 FYYIYSQTYFRQOEIKENTKNDKQWQYIYKYTSYPPDILMKASRNSCWSKAEYGLY 240
DB 181 FYYIYSQTYFRQOEIKENTKNDKQWQYIYKYTSYPPDILMKASRNSCWSKAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSYTNEHLIDMDHESFPGATLVG 281
DB 241 SIYOGIFELKENDRIFVSYTNEHLIDMDHESFPGATLVG 281

RESULT 6
AAW44354
ID AAW44354 standard; protein; 281 AA.
XX
XX AAW44354;
AC
XX
XX 28-MAY-1998 (first entry)
DT
XX
XX Human AGP-1.
DE
XX
XX Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
KW bone resorption; haematopoietic disease.
XX
XX Homo sapiens.
OS
XX
XX WO9746686-A2.
PN
XX 11-DEC-1997.
PD
XX
XX 06-JUN-1997; 97WO-US009895.
PF
XX 07-JUN-1996; 96US-00660562.
PR
XX (AMGE-) AMGEN INC.
PA
XX Johnson MJ, Simonet WS, Danilenko DM;
PI
XX WPI; 1998-042194/04.
DR N-PSDB; AAV15295.
XX
XX Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
PT useful for treating inflammation, bone resorption and haematopoietic
PT diseases.
XX
XX Claim 7; Page 36-37; 54pp; English.
XX
XX The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
CC factor (TNF)-related protein, involved in inflammation, myelopoiesis and
CC bone resorption. It has the same nucleic acid and amino acid (aa)
CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
CC haematopoietic diseases associated with reduction in the number of bone
CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
CC by disease, injury or exposure to myelosuppressive agents. Host cells,
CC transformed with expression vectors containing AGP-1 DNA, are used to
CC produce recombinant AGP-1
CC
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGSPSLGQTCVLIVFTVLLQSLCAVATVYVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGSPSLGQTCVLIVFTVLLQSLCAVATVYVYFTNELKQMDKYSKSGIACFLKE 60

```


QY 61 DSDYNDPNDDESMNSPCQVKKQLRQVYRKMLRTSEETISTVQEKQONISPLVERBQ 120
 DB 61 DSDYNDPNDDESMNSPCQVKKQLRQVYRKMLRTSEETISTVQEKQONISPLVERBQ 120
 QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRPQBEIKENTKNDKQVQIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRPQBEIKENTKNDKQVQIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 7
 ID AAY01517 standard; peptide; 281 AA.
 AC AAY01517;
 DT 27-MAY-1999 (first entry)

DE Protein associated with neurodegenerative and autoimmune diseases.
 XX Neurodegenerative disease; autoimmune disease; inflammatory disease;
 KM lupus erythematosus; rheumatoid arthritis; SFP; apoptotic;
 XX surface receptor; TRAIL protein.

OS Homo sapiens.
 XX FR276713-A1.
 XX 05-FEB-1999.
 XX 04-AUG-1997; 97FR-00010176.
 XX 04-AUG-1997; 97FR-00010176.
 XX 04-AUG-1997; 97FR-00010176.

XX (INMR) BIO MERIEUX.
 XX Rieger F, Belliveau JF, Perron H;
 XX WPI; 1999-156177/14.

PT Use of polypeptide derived from TRAIL protein for diagnosis of
 PT degenerative disease - autoimmunity and inflammation, also useful in
 PT prevention or treatment, and similar use of corresponding ligand and
 PT nucleic acid.

PS Claim 2; Page 13; 21pp; French.

XX The specification describes the use of a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative diseases, lupus erythematosus,
 CC rheumatoid arthritis, and SFP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVIFVTLQSLCVAVTYYVFTNELKQMDKXSKSGIACFLKE 60

DB 1 MAMMEVQGGPSLQGTCLVIFVTLQSLCVAVTYYVFTNELKQMDKXSKSGIACFLKE 60
 QY 61 DSDYNDPNDDESMNSPCQVKKQLRQVYRKMLRTSEETISTVQEKQONISPLVERBQ 120
 DB 61 DSDYNDPNDDESMNSPCQVKKQLRQVYRKMLRTSEETISTVQEKQONISPLVERBQ 120
 QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRPQBEIKENTKNDKQVQIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRPQBEIKENTKNDKQVQIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 8
 ID AAY27012 standard; protein; 281 AA.
 AC AAY27012;
 DT 24-SEP-1999 (first entry)

DE Human Apo-2 ligand (Apo-2L) polypeptide.

XX Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
 KM lupus; immune-mediated glomerular nephritis; human.

XX Homo sapiens.
 XX WO9936535-A1.
 XX 22-JUL-1999.
 XX 15-JAN-1999; 99WO-US001039.
 XX 15-JAN-1999; 98US-00007886.
 XX 15-APR-1998; 98US-00060533.

XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Kelley RF, O'Connell MT, Plicci RM, Schwall RH;
 XX WPI; 1999-44397/37.
 XX N-PSDB; AAX86987.

PT A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 PT in mammalian cancer cells.

PS Claim 1; Fig 1A; 86pp; English.

XX This sequence represents a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MAMMEVQGSPSLGQTCVLIVITFTVLLQSLCAVATVYVYFTNELKQMDKXSKSGIACFLKE 60
DB 1 MAMMEVQGSPSLGQTCVLIVITFTVLLQSLCAVATVYVYFTNELKQMDKXSKSGIACFLKE 60
QY 61 DSYNDPNDDEESMNSPCQVQKQOLRVLRKMLRTSEETISTVOEKQONISPLVBERGQ 120
DB 61 DSYNDPNDDEESMNSPCQVQKQOLRVLRKMLRTSEETISTVOEKQONISPLVBERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEBIKENTKDKQMVQYIYKTYSPDPILMKSAKNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEBIKENTKDKQMVQYIYKTYSPDPILMKSAKNSCWSKDAEYGLY 240
QY 241 STYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 STYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 9
AAY81956
ID AAY81956 standard; protein; 281 AA.
XX
XX AAY81956;
AC
XX
DT 10-JUL-2000 (first entry)
XX
DE Human Apo-2 ligand protein sequence.
XX
XX Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
XX KW therapy; apoptosis; cancer.
XX
XX OS Homo sapiens.
XX
XX US6046048-A.
XX
XX PD 04-APR-2000.
XX
XX PF 08-JAN-1997; 97US-00780496.
XX
XX PR 09-JAN-1996; 96US-0009755P.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Kim KJ, Ashkenazi AJ, Chuntharapai A;
XX
XX DR WPI; 2000-282690/24.
XX
XX DR N-PSDB; AAA07425.
XX
XX PT New isolated monoclonal antibodies having antigen specificity for Apo-2
XX PT ligand, e.g. 2G6, 2B11 or 5G2, useful for detecting the expression of Apo
XX PT -2 ligand serum, and for treating diseases associated with increased
XX PT apoptosis.
XX
XX PS Claim 9; Fig 1a; 46bp; English.
XX
XX CC This sequence is the human Apo-2 ligand protein, which is recognised by
XX CC monoclonal antibodies produced by the hybridoma cell lines of the
XX CC invention. The hybridoma cell lines are deposited under the American Type
XX CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
XX CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
XX CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
XX CC tissues, or serum. The antibodies may also be employed as therapeutics.
XX CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
XX CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
XX CC pathological conditions or diseases associated with increased apoptosis.
XX CC They are also useful for the affinity purification of Apo-2 ligand from
XX CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
XX CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells
XX
XX SQ Sequence 281 AA;
```

```
Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGSPSLGQTCVLIVITFTVLLQSLCAVATVYVYFTNELKQMDKXSKSGIACFLKE 60
DB 1 MAMMEVQGSPSLGQTCVLIVITFTVLLQSLCAVATVYVYFTNELKQMDKXSKSGIACFLKE 60
QY 61 DSYNDPNDDEESMNSPCQVQKQOLRVLRKMLRTSEETISTVOEKQONISPLVBERGQ 120
DB 61 DSYNDPNDDEESMNSPCQVQKQOLRVLRKMLRTSEETISTVOEKQONISPLVBERGQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEBIKENTKDKQMVQYIYKTYSPDPILMKSAKNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEBIKENTKDKQMVQYIYKTYSPDPILMKSAKNSCWSKDAEYGLY 240
QY 241 STYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 STYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 10
AAB24038
ID AAB24038 standard; protein; 281 AA.
XX
XX AAB24038;
AC
XX
DT 25-JAN-2001 (first entry)
XX
DE Human PRO1096 protein sequence SEQ ID NO:51.
XX
XX KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
XX KW identification; tumorigenesis; anticancer; detection.
XX
XX OS Homo sapiens.
XX
XX WO200053750-A1.
XX
XX PN 14-SEP-2000.
XX
XX PD 02-DEC-1999; 99WO-US028551.
XX
XX PF 08-MAR-1999; 99WO-US005028.
XX
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 29-OCT-1999; 99US-0162506P.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1999; 99WO-US028634.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WT;
XX
XX DR WPI; 2000-594320/56.
XX
XX DR N-PSDB; AAC58120.
XX
XX PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit
XX PT the growth of tumors in mammals, and to identify inhibitors of PRO
XX PT polypeptide activity or expression.
XX
XX PS Claim 61; Fig 36; 226bp; English.
XX
XX CC The present invention describes an antibody that binds to a human protein
XX CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
XX CC PRO1927; PRO1567; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
XX CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
XX CC activity and can be used to diagnose tumours in mammals, by detecting
XX CC complex formation when the antibody is contacted with test cells.
XX CC Increased expression of genes encoding (I) can also be detected to
```

CC diagnose tumours. Agents which inhibit the activity of (I), especially
 CC the antibodies, or an antisense oligonucleotide which hybridises to genes
 CC encoding (I), can be used to inhibit tumour growth, preferably by
 CC inducing cell death. Methods from the present invention can be used to
 CC identify compounds which inhibit the biological activity of (I). AAC58019
 CC to AAC58102 represent PCR primers and hybridisation probes used in
 CC examples from the present invention for human PRO sequences. AAC58103 to
 CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
 CC protein sequences given in the exemplification of the present invention
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKXSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKXSKSGIACFLKE 60
 QY 61 DDSYWDPNDEBSMNSPCQVQKQLRQLVRKMLRTSEETISTVOEKQONISPLVERGPQ 120
 DB 61 DDSYWDPNDEBSMNSPCQVQKQLRQLVRKMLRTSEETISTVOEKQONISPLVERGPQ 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWSSRSRSGHSFLSNLHRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWSSRSRSGHSFLSNLHRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVYG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVYG 281

RESULT 11

AAB08545
 ID AAB08545 standard; protein; 281 AA.

AC AAB08545;

DT 20-DEC-2000 (first entry)

DE Amino acid sequence of a human TRAIL polypeptide.

KW Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;

KW TNF related apoptosis-inducing ligand; tumour cell;

KW TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;

KW non-small cell lung carcinoma.

OS Homo sapiens.

PN WO200048619-A1.

PD 24-AUG-2000.

PF 15-FEB-2000; 2000WO-US003891.

PR 16-FEB-1999; 99US-0120313P.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Rosen GD;

DR MPI: 2000-558253/51.

DR N-PSDB; AAA64325.

XX Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
 PT administration of synergistic combination of diterpenoid diepoxide and
 PT tumor necrosis factor related apoptosis-inducing ligand.
 XX

PS Disclosure; Page 23-24; 29pp; English.

XX The present sequence represents a human TRAIL (tumour necrosis factor
 CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification
 CC describes a method for enhanced killing of tumour cells. The method
 CC comprises contacting a susceptible tumour cell with a synergistic mixture
 CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
 CC dosage to kill at least 50 % of the cells. This mixture is synergistic,
 CC and so is active at lower doses and against otherwise resistant cell
 CC lines. The method is used for killing tumour cells, especially solid
 CC tumours or carcinomas (especially mammary carcinoma or non-small cell
 CC lung carcinoma)
 XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKXSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKXSKSGIACFLKE 60
 QY 61 DDSYWDPNDEBSMNSPCQVQKQLRQLVRKMLRTSEETISTVOEKQONISPLVERGPQ 120
 DB 61 DDSYWDPNDEBSMNSPCQVQKQLRQLVRKMLRTSEETISTVOEKQONISPLVERGPQ 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWSSRSRSGHSFLSNLHRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWSSRSRSGHSFLSNLHRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVYG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVYG 281

RESULT 12

AAB28691
 ID AAB28691 standard; protein; 281 AA.

AC AAB28691;

DT 14-FEB-2001 (first entry)

DE Human AGP-1.

KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;

KW antiinflammatory; hepatocytic; antiarteriosclerotic; anti-HIV; HIV;

KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;

KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;

KW transplant rejection; cardiovascular disease; arteriosclerosis.

OS Homo sapiens.

PN WO200063253-A1.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US008004.

PR 16-APR-1999; 99US-00293245.

PA (AMGE-) AMGEN INC.

PI Hsu H, Meng S;

DR MPI: 2000-665240/64.

DR N-PSDB; AAC67831.

PT Fusion protein of Agp-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced disorders.
XX
XX Claim 3; Fig 2; 93pp; English.
XX
CC The present sequence is human Agp-1, a type II transmembrane protein.
CC Fusion protein comprising an Fc immunoglobulin region fused to the N-
CC terminal portion of the Agp-1 protein have been produced. The fusion
CC proteins can be used to induce apoptosis in a tissue, and to treat
CC proliferative disorders, immune disorders, or virally-induced disorders.
CC The proliferative disorders include cancers, such as breast, prostate,
CC lung or colon cancer. The viral infections include hepatitis, and
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC such as arteriosclerosis may also be treated. The Agp-1 containing fusion
CC proteins have increased biological activity compared to the soluble Agp-1
CC proteins used in prior art therapies
XX
SQ Sequence 281 AA:
Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGSPSLGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKGIACPKX 60
DB 1 MAMMEVQGSPSLGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKGIACPKX 60
QY 61 DSYWDPNDEESMNSPCQVQKQOLVLRKMLRTSEETSTVQKQONISPLVERGQ 120
DB 61 DSYWDPNDEESMNSPCQVQKQOLVLRKMLRTSEETSTVQKQONISPLVERGQ 120
QY 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYPPDPLLMKSAKNSCWDKAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYPPDPLLMKSAKNSCWDKAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 13
AAB50977
ID AAB50977 standard; protein; 281 AA.
XX
AC AAB50977;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO1096 protein.
XX
KW Human; PRO; cytosolic; neutrotropic; neuroprotective; respiratory general;
KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
XX
OS Homo sapiens.
XX
PN WO200073348-A2.
XX
PD 07-DEC-2000.
XX
PF 30-MAY-2000; 2000WO-US014941.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.

PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
XX Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
XX WPI, 2001-016509/02.
XX N-PSDB; AAC91579.
XX
PT Twenty eight nucleic acids encoding PRO polypeptides which are useful for
PT treating various tumors, e.g. breast cancer, and other inflammatory,
PT angiogenic and immunological disorders.
XX
XX Claim 31; Fig 54; 188pp; English.
XX
CC The present sequence is one of twenty eight novel PRO polypeptides. The
CC PRO polypeptides and their agonists, including antibodies, peptides, and
CC small molecule agonists, may be used to treat various tumors, e.g.,
CC cancers such as breast cancer, prostate cancer, lung cancer, bladder cancer,
CC cancer, uterine cancer, ovarian cancer, renal cancer, colorectal
CC central nervous system cancer, melanoma or leukemia. They are also
CC useful for treating other disorders such as neuronal, glial, astrocytal,
CC hypocoelamic and other glandular, macrophagal, epithelial, stromal and
CC blastocellic disorders, and inflammatory, angiogenic and immunological
CC disorders
XX
SQ Sequence 281 AA:
Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGSPSLGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKGIACPKX 60
DB 1 MAMMEVQGSPSLGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKXSKGIACPKX 60
QY 61 DSYWDPNDEESMNSPCQVQKQOLVLRKMLRTSEETSTVQKQONISPLVERGQ 120
DB 61 DSYWDPNDEESMNSPCQVQKQOLVLRKMLRTSEETSTVQKQONISPLVERGQ 120
QY 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYPPDPLLMKSAKNSCWDKAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYPPDPLLMKSAKNSCWDKAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 14
AAB67243
ID AAB67243 standard; protein; 281 AA.

```

XX AC AAB67243;
XX 18-APR-2001 (first entry)
XX DE Human Apo2 ligand.
XX KM Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
XX OS Homo sapiens.
XX PN WO200100832-A1.
XX PD 04-JAN-2001.
XX PF 26-JUN-2000; 2000WO-US017579.
XX PR 28-JUN-1999; 99US-0141342P.
XX PA (GENTH ) GENENTECH INC.
XX PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
XX O'Connell M, Pai R, Shahrokhi Z, Simmons L;
XX WPI; 2001-123012/13.
XX DR Use of divalent metal ions for making Apo-2 ligand and in formulations
XX PT containing Apo-2 ligand for increasing yield and stability of ligand
XX PT trimers, useful for therapeutic applications.
XX PS Claim 6; Fig 1; 60pp; English.
XX CC The present invention relates to a formulation comprising Apo-2 ligand
XX CC and divalent metal ions. Apo-2 ligand and the formulation are useful for
XX CC treating cancers and viral infections. Addition of divalent metal ions
XX CC for making Apo-2 ligand and formulations containing Apo-2 ligand results
XX CC in increased yield and stability of Apo-2 ligand trimers
XX SQ Sequence 281 AA;

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKSKSGIACFLKE 60
QY 61 DSYMDPNDDEESMNSPCQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVERGPO 120
DB 61 DSYMDPNDDEESMNSPCQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVERGPO 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYISQTYFRROEIKENTKNDKQVQIYIKTSTPDPILMLKSRNSGSKDAEYGLY 240
DB 181 FYIYISQTYFRROEIKENTKNDKQVQIYIKTSTPDPILMLKSRNSGSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 15
AAE11031
ID AAE11031 standard; protein; 281 AA.
XX AAE11031;
AC AAE11031;
XX 18-DEC-2001 (first entry)
XX DT
XX

```

```

DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
XX Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
XX TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
XX human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
XX melanoma.
XX OS Homo sapiens.
XX PN US6284236-B1.
XX PD 04-SEP-2001.
XX PF 26-MAY-1999; 99US-00320424.
XX PR 29-JUN-1995; 95US-0049632.
XX PR 01-NOV-1995; 95US-00548368.
XX PR 25-JUN-1996; 96US-00670354.
XX PR 26-MAR-1998; 98US-00048641.
XX PR 10-NOV-1998; 98US-00190046.
XX PA (IMMUNEX ) IMMUNEX CORP.
XX PI Wiley SR, Goodwin RG;
XX WPI; 2001-595463/67.
XX DR N-PSDB; AAD18395.
XX PT New tumor necrosis factor related apoptosis inducing ligand polypeptides
XX PT for treating viral infections (e.g. bovine viral diarrhoea or human
XX PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
XX PS Claim 2; Col 45-48; 41pp; English.
XX CC The invention relates to a cytokine designated as tumour necrosis factor
XX CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
XX CC of certain target cells, including cancer cells and virally infected
XX CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
XX CC treating viral infections (e.g. bovine viral diarrhoea or human
XX CC immunodeficiency virus (HIV) and cancers (e.g. leukaemia, lymphoma and
XX CC melanoma), as a research reagent useful in studying apoptosis including
XX CC the regulation of programmed cell death. TRAIL DNA sequences may be
XX CC employed in developing a gene therapy approach to treating disorders
XX CC mediated by defective or insufficient amounts of TRAIL, in the production
XX CC of TRAIL polypeptides and as probes or primers in polymerase chain
XX CC reactions (PCR). The present sequence is human TRAIL protein
XX SQ Sequence 281 AA;

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKSKSGIACFLKE 60
QY 61 DSYMDPNDDEESMNSPCQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVERGPO 120
DB 61 DSYMDPNDDEESMNSPCQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVERGPO 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180

```

| | | | |
|----|-----|---|-----|
| Qy | 181 | FYYISQTYFRFOEIKENTKNDKQWQYIYKYTSYPPILMKSARNSCWSKDAEYGLY | 240 |
| Db | 181 | FYYISQTYFRFOEIKENTKNDKQWQYIYKYTSYPPILMKSARNSCWSKDAEYGLY | 240 |
| Qy | 241 | SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLVG | 281 |
| Db | 241 | SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLVG | 281 |

Search completed: March 2, 2005, 14:47:40
Job time : 176 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 14:41:36 ; Search time 43 Seconds
(without alignments)
487.823 Million cell updates/sec

Title: US-10-077-435-1

Perfect score: 1478

Sequence: 1 MAMMEVQGSPSLGQTCVLIV.....NEHLIDMDHASFQAPLVG 281

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued Patents, AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1478 | 100.0 | 281 | 1 | US-08-670-354-2 |
| 2 | 1478 | 100.0 | 281 | 3 | US-08-584-031-1 |
| 3 | 1478 | 100.0 | 281 | 3 | US-08-780-496-1 |
| 4 | 1478 | 100.0 | 281 | 3 | US-08-883-086-10 |
| 5 | 1478 | 100.0 | 281 | 3 | US-09-320-424-2 |
| 6 | 1478 | 100.0 | 281 | 3 | US-09-333-593A-6 |
| 7 | 1478 | 100.0 | 281 | 4 | US-09-157-864-11 |
| 8 | 1478 | 100.0 | 281 | 4 | US-09-825-563-2 |
| 9 | 1478 | 100.0 | 281 | 4 | US-09-919-039-118 |
| 10 | 1478 | 100.0 | 281 | 4 | US-09-582-450-1 |
| 11 | 1478 | 100.0 | 281 | 4 | US-09-934-465-1 |
| 12 | 1478 | 100.0 | 281 | 4 | US-10-011-125A-4 |
| 13 | 1478 | 100.0 | 281 | 5 | PCT-US96-10895-2 |
| 14 | 1469 | 99.4 | 279 | 3 | US-09-072-993C-3 |
| 15 | 1238 | 83.4 | 271 | 4 | US-09-569-611C-30 |
| 16 | 988 | 66.8 | 253 | 3 | US-09-320-424-11 |
| 17 | 988 | 66.8 | 253 | 4 | US-09-825-563-11 |
| 18 | 988 | 66.8 | 256 | 3 | US-09-320-424-13 |
| 19 | 988 | 66.8 | 256 | 4 | US-09-825-563-13 |
| 20 | 930 | 62.9 | 177 | 3 | US-09-105-343A-7 |
| 21 | 930 | 62.9 | 291 | 1 | US-08-670-354-6 |
| 22 | 930 | 62.9 | 291 | 4 | US-09-320-424-6 |
| 23 | 930 | 62.9 | 291 | 4 | US-09-825-563-6 |
| 24 | 930 | 62.9 | 291 | 5 | PCT-US96-10895-6 |
| 25 | 850 | 57.5 | 161 | 4 | US-09-565-423-7 |
| 26 | 735 | 49.7 | 169 | 4 | US-09-569-611C-29 |
| 27 | 654 | 44.2 | 183 | 3 | US-09-105-343A-8 |

| | | | | | | |
|----|-------|------|-----|---|---------------------|-------------------|
| 28 | 611 | 41.3 | 121 | 4 | US-09-513-999C-7833 | Sequence 7833, Ap |
| 29 | 483 | 32.7 | 120 | 4 | US-09-569-611C-32 | Sequence 32, Appl |
| 30 | 482 | 32.6 | 101 | 1 | US-08-670-354-4 | Sequence 4, Appl |
| 31 | 482 | 32.6 | 101 | 3 | US-09-320-424-4 | Sequence 4, Appl |
| 32 | 482 | 32.6 | 101 | 4 | US-09-825-563-4 | Sequence 4, Appl |
| 33 | 482 | 32.6 | 101 | 5 | PCT-US96-10895-4 | Sequence 4, Appl |
| 34 | 482 | 32.6 | 122 | 4 | US-09-569-611C-31 | Sequence 31, Appl |
| 35 | 446 | 30.2 | 85 | 4 | US-09-633-287A-12 | Sequence 12, Appl |
| 36 | 258.5 | 17.5 | 294 | 3 | US-08-995-659-11 | Sequence 11, Appl |
| 37 | 258.5 | 17.5 | 294 | 3 | US-09-215-649A-11 | Sequence 11, Appl |
| 38 | 258.5 | 17.5 | 294 | 3 | US-09-577-780-11 | Sequence 11, Appl |
| 39 | 258.5 | 17.5 | 294 | 4 | US-09-466-496-11 | Sequence 11, Appl |
| 40 | 258.5 | 17.5 | 294 | 4 | US-09-466-496-11 | Sequence 11, Appl |
| 41 | 258.5 | 17.5 | 294 | 4 | US-09-871-856-11 | Sequence 11, Appl |
| 42 | 258.5 | 17.5 | 294 | 4 | US-09-871-856-11 | Sequence 11, Appl |
| 43 | 258.5 | 17.5 | 294 | 4 | US-09-871-856-11 | Sequence 11, Appl |
| 44 | 258.5 | 17.5 | 294 | 4 | US-09-877-650-11 | Sequence 11, Appl |
| 45 | 258.5 | 17.5 | 294 | 4 | US-09-865-363-11 | Sequence 11, Appl |

ALIGNMENTS

RESULT 1
US-08-670-354-2
Sequence 2, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-354-2
Query Match 100.0%; Score 1478; DB 1; Length 281;

[illegible]

```

RESULT 2
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Av4 J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-584-031-1

```

[illegible]

```

RESULT 3
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntcharapai, Kyung Jin Kim

```

```

1  TITLE OF INVENTION: Apo-2 Ligand
2  NUMBER OF SEQUENCES: 8
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE: Genentech, Inc.
5  STREET: 460 Point San Bruno Blvd
6  CITY: South San Francisco
7  STATE: California
8  COUNTRY: USA
9  ZIP: 94080
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Winpatin (Genentech)
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/780,496
17 FILING DATE: 08-Jan-1997
18 CLASSIFICATION: 435
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Marchand, Diane L.
21 REGISTRATION NUMBER: 35,600
22 REFERENCE/DOCKET NUMBER: P0978P1
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 415/952-5416
25 TELEFAX: 415/952-9281
26 TELEX: 910/371-7168
27 INFORMATION FOR SEQ ID NO: 1:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 281 amino acids
30 TYPE: Amino Acid
31 TOPOLOGY: Linear
32 /S-08-780-496-1

```

| | | | | |
|---------------------------|---------|---------------------|-------|------------------|
| Query Match | 100.0%; | Score 1478; | DB 3; | Length 281; |
| Best Local Similarity | 100.0%; | Pred. No. 3.5e-149; | | |
| Matches 281; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0 |

| | | | |
|----|-----|--|-----|
| QY | 1 | MAMMEVQGGPSLGGQICVLIVFTVLLGSLCAVAVTVVETNELKQMDKYSKSGIACPLKE | 60 |
| QY | 1 | MAMMEVQGGPSLGGQICVLIVFTVLLGSLCAVAVTVVETNELKQMDKYSKSGIACPLKE | 60 |
| Db | 1 | MAMMEVQGGPSLGGQICVLIVFTVLLGSLCAVAVTVVETNELKQMDKYSKSGIACPLKE | 60 |
| QY | 61 | DDSYMDPNDESMNSPCWQVKKQOLRQVLRKMLILTSEETISTVQEKQONISPLVERGPQ | 120 |
| Db | 61 | DDSYMDPNDESMNSPCWQVKKQOLRQVLRKMLILTSEETISTVQEKQONISPLVERGPQ | 120 |
| QY | 121 | RYAAAHITGRGSSNTLSSPNSKNKEALARKXINSMESSSGHSFJSLNHLRNGELVIREHG | 180 |
| Db | 121 | RYAAAHITGRGSSNTLSSPNSKNKEALARKXINSMESSSGHSFJSLNHLRNGELVIREHG | 180 |
| QY | 121 | RYAAAHITGRGSSNTLSSPNSKNKEALARKXINSMESSSGHSFJSLNHLRNGELVIREHG | 180 |
| Db | 121 | RYAAAHITGRGSSNTLSSPNSKNKEALARKXINSMESSSGHSFJSLNHLRNGELVIREHG | 180 |
| QY | 181 | FYYIYSQYIFRPQBEIKENTKNDKQMDQVYIKYTSYDPDILMLKSARNSCMSKDAEYGLY | 240 |
| Db | 181 | FYYIYSQYIFRPQBEIKENTKNDKQMDQVYIKYTSYDPDILMLKSARNSCMSKDAEYGLY | 240 |
| QY | 241 | SIYQGGIFELKENDRIFVSVTNEHLLIMDDHASPFGAFLVG | 281 |
| Db | 241 | SIYQGGIFELKENDRIFVSVTNEHLLIMDDHASPFGAFLVG | 281 |

RESULT 4
 US-08-883-086-10
 ; Sequence 10, Application US/08883086
 ; Patent No. 6171787
 ; GENERAL INFORMATION:
 ; APPLICANT: WILEY, STEVEN
 ; TITLE OF INVENTION: MEMBER OF THE TNP FAMILY USEFUL
 ; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASES
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA

ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/883,086
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Porembek, Priscilla E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 6134.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-937-0378
 TELEFAX: 847-938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6171787e
 US-08-883-086-10

Query Match 100.0%; Score 1478; DB 3; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.5e-149; Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKXSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKXSKSGIACFLKE 60
 QY 61 DDSYDNDPDEESMSPCQVQKQQLRQVVKMLRTSEETISTVOEKQONISPLVERGPQ 120
 DB 61 DDSYDNDPDEESMSPCQVQKQQLRQVVKMLRTSEETISTVOEKQONISPLVERGPQ 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKASRNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKASRNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 5

US-09-320-424-2

Sequence 2, Application US/09320424
 Patent No. 6284236
 GENERAL INFORMATION:
 APPLICANT: Wiley, Steven R.
 APPLICANT: Goodwin, Raymond G.
 TITLE OF INVENTION: Cytokine that Induces Apoptosis
 FILE REFERENCE: 2835-E
 CURRENT APPLICATION NUMBER: US/09/320,424
 PRIOR FILING DATE: 1999-05-26
 EARLIER APPLICATION NUMBER: 09/190,046
 PRIOR FILING DATE: 1998-11-10
 EARLIER APPLICATION NUMBER: 09/048,641
 EARLIER FILING DATE: 1998-03-26
 EARLIER APPLICATION NUMBER: 08/670,354
 EARLIER FILING DATE: 1996-06-25
 EARLIER APPLICATION NUMBER: 08/548,368

EARLIER FILING DATE: 1995-11-01
 EARLIER APPLICATION NUMBER: 08/496,632
 EARLIER FILING DATE: 1995-06-29
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 2:
 LENGTH: 281
 TYPE: PRT
 ORGANISM: human
 US-09-320-424-2

Query Match 100.0%; Score 1478; DB 3; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.5e-149; Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKXSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKXSKSGIACFLKE 60
 QY 61 DDSYDNDPDEESMSPCQVQKQQLRQVVKMLRTSEETISTVOEKQONISPLVERGPQ 120
 DB 61 DDSYDNDPDEESMSPCQVQKQQLRQVVKMLRTSEETISTVOEKQONISPLVERGPQ 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKASRNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKASRNSCWSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 6

US-09-333-593A-6

Sequence 6, Application US/09333593A
 Patent No. 6313269
 GENERAL INFORMATION:
 APPLICANT: DEEN, KEITH C.
 APPLICANT: YOUNG, PETER R.
 APPLICANT: MARSHALL, LISA A.
 APPLICANT: ROSHAK, AMY K.
 APPLICANT: TAN, KONG B.
 APPLICANT: TRUNER, ALEMESEGED
 TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
 FILE REFERENCE: TR6
 CURRENT APPLICATION NUMBER: US/09/333,593A
 PRIOR FILING DATE: 1999-06-15
 PRIOR APPLICATION NUMBER: 08/916,625
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 08/853,684
 PRIOR FILING DATE: 1997-05-09
 PRIOR APPLICATION NUMBER: 60/041,230
 PRIOR FILING DATE: 1997-03-14
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 6
 LENGTH: 281
 TYPE: PRT
 ORGANISM: HOMO SAPIENS
 US-09-333-593A-6

Query Match 100.0%; Score 1478; DB 3; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.5e-149; Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKXSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKXSKSGIACFLKE 60

QY 61 DSDYDNDPDEESMNSPCWQVQWOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
DB 61 DSDYDNDPDEESMNSPCWQVQWOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSARNSCWSKDAEYGLY 240
DB 181 FYYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 7
US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-09-157-864-11

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAMEEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
DB 1 NAMEEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
QY 61 DSDYDNDPDEESMNSPCWQVQWOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
DB 61 DSDYDNDPDEESMNSPCWQVQWOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120

QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSARNSCWSKDAEYGLY 240
DB 181 FYYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 8
US-09-825-563-2
; Sequence 2, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-825-563-2

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAMEEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
DB 1 NAMEEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
QY 61 DSDYDNDPDEESMNSPCWQVQWOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
DB 61 DSDYDNDPDEESMNSPCWQVQWOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
QY 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGNSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSARNSCWSKDAEYGLY 240
DB 181 FYYISQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 9
US-09-919-039-118
; Sequence 118, Application US/09919039

```

; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaeet, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
US-09-919-039-118

```

```

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYMDPNDDESMNSPCWQVKQQLRQLVAKMLRTSEETISTVQEKQONISPLVREGRQ 120
DB 61 DSDYMDPNDDESMNSPCWQVKQQLRQLVAKMLRTSEETISTVQEKQONISPLVREGRQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSLHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSLHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

```

```

RESULT 10
US-09-582-450-1
; Sequence 1, Application US/09582450
; Patent No. 6740739

```

```

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Kelley, Robert F.
; APPLICANT: O'Connell, Mark P.
; APPLICANT: Plichi, Robert M.
; APPLICANT: Schwall, Ralph H.
; TITLE OF INVENTION: Apo-2 Ligand
; FILE REFERENCE: P0978P4
; CURRENT APPLICATION NUMBER: US/09/582,450
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/007,886
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 09/060,533
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-450-1

```

```

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYMDPNDDESMNSPCWQVKQQLRQLVAKMLRTSEETISTVQEKQONISPLVREGRQ 120
DB 61 DSDYMDPNDDESMNSPCWQVKQQLRQLVAKMLRTSEETISTVQEKQONISPLVREGRQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSLHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSLHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

```

```

RESULT 11
US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. 6746668

```

```

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 Ligand
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

```

```

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSDYMDPNDDESMNSPCWQVKQQLRQLVAKMLRTSEETISTVQEKQONISPLVREGRQ 120
DB 61 DSDYMDPNDDESMNSPCWQVKQQLRQLVAKMLRTSEETISTVQEKQONISPLVREGRQ 120
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSLHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSLHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

```

```

RESULT 12
US-10-011-125A-4
; Sequence 4, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching

```

;/ TITLE OF INVENTION: BACTERIAL HOST STRAINS
;/ FILE REFERENCE: P1804R1
;/ CURRENT APPLICATION NUMBER: US/10/011,125A
;/ CURRENT FILING DATE: 2001-12-07
;/ PRIOR APPLICATION NUMBER: US 60/256,162
;/ PRIOR FILING DATE: 2000-12-14
;/ NUMBER OF SEQ ID NOS: 12
;/ SEQ ID NO 4
;/ LENGTH: 281
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
US-10-011-125A-4

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSGIACFLKE 60
QY 61 DSDYMDPNDEESMNSPCWQVKMQLRVKRMILRTSEETISTVOEKQONISPLVERGPQ 120
DB 61 DSDYMDPNDEESMNSPCWQVKMQLRVKRMILRTSEETISTVOEKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKTSYDPDILMKSAARNSCWDKAEYGLY 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKTSYDPDILMKSAARNSCWDKAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 13

PCT-US96-10895-2
Sequence 2, Application PC/TUS9610895

;/ GENERAL INFORMATION:
;/ APPLICANT: Immunex Corporation.
;/ TITLE OF INVENTION: Cyclokin That Induces Apoptosis
;/ NUMBER OF SEQUENCES: 9
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
;/ STREET: 51 University Street
;/ CITY: Seattle
;/ STATE: WA
;/ COUNTRY: USA
;/ ZIP: 98101
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: Apple Macintosh
;/ OPERATING SYSTEM: Apple 7.5.2
;/ SOFTWARE: Microsoft Word, Version 6.0.1
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US96/10895
;/ FILING DATE: 25-JUN-1996
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/496,632
;/ FILING DATE: 29-JUN-1995
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/548,368
;/ FILING DATE: 01-NOV-1995
;/ CLASSIFICATION:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Anderson, Kathryn A.
;/ REGISTRATION NUMBER: 32,172
;/ REFERENCE/DOCKET NUMBER: 2835-WO

;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (206) 587-0430
;/ TELEFAX: (206) 233-0644
;/ TELEX: 756822
;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 281 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match 100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSGIACFLKE 60
QY 61 DSDYMDPNDEESMNSPCWQVKMQLRVKRMILRTSEETISTVOEKQONISPLVERGPQ 120
DB 61 DSDYMDPNDEESMNSPCWQVKMQLRVKRMILRTSEETISTVOEKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKTSYDPDILMKSAARNSCWDKAEYGLY 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKTSYDPDILMKSAARNSCWDKAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 14

US-09-072-993C-3
Sequence 3, Application US/09072993C

;/ GENERAL INFORMATION:
;/ APPLICANT: Michael R. Brigham-Burke
;/ APPLICANT: Peter R. Young
;/ TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
;/ TITLE OF INVENTION: ANTAAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
;/ FILE REFERENCE: GH-50030
;/ CURRENT APPLICATION NUMBER: US/09/072,993C
;/ CURRENT FILING DATE: 1998-05-06
;/ PRIOR APPLICATION NUMBER: 60/055,513
;/ PRIOR FILING DATE: 1997-08-13
;/ PRIOR APPLICATION NUMBER: 60/056,980
;/ PRIOR FILING DATE: 1997-08-26
;/ PRIOR APPLICATION NUMBER: 60/057,550
;/ PRIOR FILING DATE: 1997-08-29
;/ NUMBER OF SEQ ID NOS: 9
;/ SOFTWARE: FastSeq for Windows Version 3.0
;/ SEQ ID NO 3
;/ LENGTH: 279
;/ TYPE: PRT
;/ ORGANISM: HOMO SAPIENS
US-09-072-993C-3

Query Match 99.4%; Score 1469; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 3.1e-148;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSGIACFLKEDD 62
DB 1 MMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSGIACFLKEDD 60
QY 63 SYMDPNDEESMNSPCWQVKMQLRVKRMILRTSEETISTVOEKQONISPLVERGPQRY 122

Db 61 SYMDPNDEESMNSPCWQVWKQLRQLVRKMLRTSEETISTVQEKQNISPLVREGRQPV 120
QY 123 AAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFY 182
Db 121 AAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFY 180
QY 183 YIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAARNSCWSDAEYGLYSI 242
Db 181 YIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAARNSCWSDAEYGLYSI 240
QY 243 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLVG 281
Db 241 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLVG 279

RESULT 15
US-09-569-611C-30
; Sequence 30, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-30

Query Match 83.8%; Score 1238; DB 4; Length 271;
Best Local Similarity 85.4%; Pred. No. 1,3e-123;
Matches 240; Conservative 2; Mismatches 5; Indels 34; Gaps 2;

QY 1 MAMMEVQGGPSLGGTCVLIVIFTVLLQSLCAVATVYVYFTNELKOMQDKYSKGIACFLKE 60
Db 25 MAMMEVQGGPSLGGTCVLIVIFTVLLQSLCAVATVYVYFTNELKOMQDKYSKGIACFLKE 84
QY 61 DDSYMDPNDEESMNSPCWQVWKQLRQLVRKMLRTSEETISTVQEKQNISPLVREGRQV 120
Db 85 DDSYMDPNDEESMNSPCWQVWKQLRQLVRK-----KSNKIFLPLVREGRQV 130
QY 121 RVAHAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
Db 131 RVAHAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 190
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAARNSCWSDAEYGLY 240
Db 191 FYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPPDILMKSAARNSCWSDAEYGLY 250
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLVG 281
Db 251 SIYOG-----IDMDHEASFGAPLVG 271

Search completed: March 2, 2005, 14:52:32
Job time : 52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 14:47:47 ; Search time 143 Seconds
(without alignments)
644.619 Million cell updates/sec

Title: US-10-077-435-1

Perfect score: 1478

Sequence: 1 MAMMEVGGSPSLGQTCVLIV.....NEHLIDMHGASFFGAPLVG 281

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 32804528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1478 | 100.0 | 281 | 8 | US-08-916-625B-6 |
| 2 | 1478 | 100.0 | 281 | 9 | US-08-921-317A-8 |
| 3 | 1478 | 100.0 | 281 | 9 | US-09-813-329-17 |
| 4 | 1478 | 100.0 | 281 | 9 | US-09-193-663-8 |
| 5 | 1478 | 100.0 | 281 | 9 | US-09-934-465-1 |
| 6 | 1478 | 100.0 | 281 | 10 | US-09-919-039-118 |
| 7 | 1478 | 100.0 | 281 | 13 | US-10-011-125-4 |
| 8 | 1478 | 100.0 | 281 | 13 | US-10-001-054-54 |
| 9 | 1478 | 100.0 | 281 | 14 | US-10-093-766-54 |
| 10 | 1478 | 100.0 | 281 | 14 | US-10-174-654-11 |
| 11 | 1478 | 100.0 | 281 | 14 | US-10-151-882-41 |
| 12 | 1478 | 100.0 | 281 | 14 | US-10-218-547-20 |
| 13 | 1478 | 100.0 | 281 | 14 | US-10-322-673-72 |

| | | | | | | |
|----|--------|-------|-----|----|-------------------|-------------------|
| 14 | 1478 | 100.0 | 281 | 14 | US-10-139-785-66 | Sequence 66, Appl |
| 15 | 1478 | 100.0 | 281 | 14 | US-10-310-793-26 | Sequence 26, Appl |
| 16 | 1478 | 100.0 | 281 | 15 | US-10-279-687-8 | Sequence 8, Appl |
| 17 | 1478 | 100.0 | 281 | 15 | US-10-292-486-5 | Sequence 5, Appl |
| 18 | 1478 | 100.0 | 281 | 15 | US-10-333-712-1 | Sequence 1, Appl |
| 19 | 1478 | 100.0 | 281 | 15 | US-10-662-429-2 | Sequence 2, Appl |
| 20 | 1478 | 100.0 | 281 | 15 | US-10-202-062-20 | Sequence 20, Appl |
| 21 | 1478 | 100.0 | 281 | 15 | US-10-662-431-2 | Sequence 2, Appl |
| 22 | 1478 | 100.0 | 281 | 15 | US-10-662-430-2 | Sequence 2, Appl |
| 23 | 1478 | 100.0 | 281 | 15 | US-10-652-244-2 | Sequence 2, Appl |
| 24 | 1478 | 100.0 | 281 | 16 | US-10-381-160-5 | Sequence 5, Appl |
| 25 | 1478 | 100.0 | 281 | 16 | US-10-755-889-210 | Sequence 210, App |
| 26 | 1478 | 100.0 | 281 | 16 | US-10-491-326-1 | Sequence 1, Appl |
| 27 | 1478 | 100.0 | 281 | 17 | US-10-771-254-1 | Sequence 1, Appl |
| 28 | 1478 | 100.0 | 281 | 17 | US-10-855-559-2 | Sequence 2, Appl |
| 29 | 1469 | 99.4 | 279 | 13 | US-10-066-209-3 | Sequence 3, Appl |
| 30 | 1456 | 98.5 | 279 | 16 | US-10-367-094-22 | Sequence 22, Appl |
| 31 | 1269.5 | 85.9 | 246 | 9 | US-09-855-544A-13 | Sequence 13, Appl |
| 32 | 1017 | 68.8 | 208 | 9 | US-09-855-544A-16 | Sequence 16, Appl |
| 33 | 988 | 66.8 | 253 | 15 | US-10-652-244-11 | Sequence 11, Appl |
| 34 | 988 | 66.8 | 256 | 15 | US-10-652-244-13 | Sequence 13, Appl |
| 35 | 985.5 | 66.7 | 461 | 15 | US-10-389-223A-6 | Sequence 6, Appl |
| 36 | 982 | 66.4 | 480 | 15 | US-10-389-223A-4 | Sequence 4, Appl |
| 37 | 978 | 66.2 | 614 | 15 | US-10-389-223A-2 | Sequence 2, Appl |
| 38 | 964.5 | 65.3 | 296 | 14 | US-10-185-425-5 | Sequence 5, Appl |
| 39 | 937.5 | 63.4 | 188 | 9 | US-09-855-544A-14 | Sequence 14, Appl |
| 40 | 930 | 62.9 | 291 | 10 | US-09-873-829-6 | Sequence 6, Appl |
| 41 | 930 | 62.9 | 291 | 13 | US-10-017-910-6 | Sequence 6, Appl |
| 42 | 930 | 62.9 | 291 | 15 | US-10-652-244-6 | Sequence 6, Appl |
| 43 | 892.5 | 60.4 | 228 | 17 | US-10-855-559-4 | Sequence 4, Appl |
| 44 | 890 | 60.2 | 287 | 16 | US-10-367-094-15 | Sequence 15, Appl |
| 45 | 887 | 60.0 | 168 | 9 | US-09-900-530A-10 | Sequence 10, Appl |

ALIGNMENTS

RESULT 1
US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication No. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATTNER & PRESTIA
; STREET: P. O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-916-625B-6

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSYNDPNDDESMNSPCQOVKQOLVRKMLRTSEETISTVQEKQONISPLVERGPQ 120
DB 61 DSYNDPNDDESMNSPCQOVKQOLVRKMLRTSEETISTVQEKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKMDAEGLY 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKMDAEGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 2
US-08-971-317A-8
Sequence 8, Application US/08971317A
Publication No. US20010010925A1

GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,317A
FILING DATE: 17-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Goller, Mimi C
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 6255.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
TELEFAX: (847) 938-2623

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-8

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSYNDPNDDESMNSPCQOVKQOLVRKMLRTSEETISTVQEKQONISPLVERGPQ 120
DB 61 DSYNDPNDDESMNSPCQOVKQOLVRKMLRTSEETISTVQEKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKMDAEGLY 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKMDAEGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 3
US-09-813-329-17

Sequence 17, Application US/09813329
Patent No. US20020012968A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 281
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-813-329-17

Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSIGQTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSYNDPNDDESMNSPCQOVKQOLVRKMLRTSEETISTVQEKQONISPLVERGPQ 120
DB 61 DSYNDPNDDESMNSPCQOVKQOLVRKMLRTSEETISTVQEKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKMDAEGLY 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQOVYIYKTSYPPDILLMKSARNSCKMDAEGLY 240

Db. 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKTYSPDILMKKSARNSCWSKDAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 4

US-09-193-663-8
; Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255 US 02
; CURRENT APPLICATION NUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-193-663-8

Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKGACFLKE 60
Db 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKGACFLKE 60
QY 61 DSDYNDPNDDESMNSPCQOVKQOLVLRKMLRTSEETISVQEKQONISPLVBERGQ 120
Db 61 DSDYNDPNDDESMNSPCQOVKQOLVLRKMLRTSEETISVQEKQONISPLVBERGQ 120
QY 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVYHEKG 180
Db 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVYHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKTYSPDILMKKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKTYSPDILMKKSARNSCWSKDAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 5

US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669,22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match 100.0%; Score 1478; DB 9; Length 281;

Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKGACFLKE 60
Db 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKGACFLKE 60
QY 61 DSDYNDPNDDESMNSPCQOVKQOLVLRKMLRTSEETISVQEKQONISPLVBERGQ 120
Db 61 DSDYNDPNDDESMNSPCQOVKQOLVLRKMLRTSEETISVQEKQONISPLVBERGQ 120
QY 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVYHEKG 180
Db 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVYHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKTYSPDILMKKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKTYSPDILMKKSARNSCWSKDAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 6

US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118

Query Match 100.0%; Score 1478; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKGACFLKE 60
Db 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCAVATVYVFTNELKQMDKXSKGACFLKE 60
QY 61 DSDYNDPNDDESMNSPCQOVKQOLVLRKMLRTSEETISVQEKQONISPLVBERGQ 120
Db 61 DSDYNDPNDDESMNSPCQOVKQOLVLRKMLRTSEETISVQEKQONISPLVBERGQ 120
QY 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVYHEKG 180
Db 121 RVAAHITGTRGNSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVYHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKTYSPDILMKKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKTYSPDILMKKSARNSCWSKDAEYGLY 240
QY 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYOGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 7

```
US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4

Query Match      100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTCVIVITFTVLQSLCAVATVYVFTNEELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGGTCVIVITFTVLQSLCAVATVYVFTNEELKQMDKYSKSGIACFLKE 60
QY 61 DDSYMDPNDEESMNSPCMQVKNQLRQLVRKMLRTSEETISTVQEKQONISPLVERGPO 120
DB 61 DDSYMDPNDEESMNSPCMQVKNQLRQLVRKMLRTSEETISTVQEKQONISPLVERGPO 120
QY 121 RVAHAHTTGRGNSNTLSSNSKQEKALGRKINSWESSRSGHSPLSNLHRLNGELVYHEKG 180
DB 121 RVAHAHTTGRGNSNTLSSNSKQEKALGRKINSWESSRSGHSPLSNLHRLNGELVYHEKG 180
QY 181 FYIYSQTYFERQOEIKENTKNDKQMVQYIYXTGYPDILMKARNSCMKDAEYGLY 240
DB 181 FYIYSQTYFERQOEIKENTKNDKQMVQYIYXTGYPDILMKARNSCMKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLVLG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLVLG 281

RESULT 8
US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austrey
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING NEOPLASTIC
; TITLE OF INVENTION: CELL GROWTH
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083545
```

```
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/096891
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096894
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100263
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/107783
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112420
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/115554
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116533
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/131294
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/218517
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/284291
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380913
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423741
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
```

PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/866034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/882636
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: PCT/US98/18824
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/US99/00106
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/08615
PRIOR FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28634
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00376
PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/06884
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/14941
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/22031
PRIOR FILING DATE: 2000-06-11
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: PCT/US01/27099
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 54
LENGTH: 281
TYPE: PRT
ORGANISM: Homo Sapien
US-10-001-054-54

Query Match 100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1,2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAMEVGGPSIGQTCVLIIVFTVLQSLCAVTVYVTTNEIKQKODKYSKSGIACFLKE 60
DB 1 NAMEVGGPSIGQTCVLIIVFTVLQSLCAVTVYVTTNEIKQKODKYSKSGIACFLKE 60
QY 61 DSYNDPDEESMNSPCQVQKQJOLVRKMLRTSEETISVQKQONISPLVERGPQ 120
DB 61 DSYNDPDEESMNSPCQVQKQJOLVRKMLRTSEETISVQKQONISPLVERGPQ 120
QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHLRNGELVIHEKG 180
DB 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHLRNGELVIHEKG 180
QY 181 FYYIISQYFRPQEBEIKENTKDKOMVOYIYKTSYPPDILMKASRNSCKMAEYGLY 240
DB 181 FYYIISQYFRPQEBEIKENTKDKOMVOYIYKTSYPPDILMKASRNSCKMAEYGLY 240
QY 241 STYGGIFELKENDRIFFVSVTNHELIDMDHEASFGALVNG 281
DB 241 STYGGIFELKENDRIFFVSVTNHELIDMDHEASFGALVNG 281

RESULT 9
US-10-093-766-54
Sequence 54, Application US/10093766
Publicatation No. US20030013099A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.
APPLICANT: Karpf, Adam R.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
FILE REFERENCE: PA-0047 US
CURRENT APPLICATION NUMBER: US/10/093,766
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
SEQ ID NO 54
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54

Query Match 100.0%; Score 1478; DB 14; Length 281;

Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELLKOMODKXSKGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELLKOMODKXSKGIACFLKE 60
Qy 61 DSDYDNDDEESMNSPCQVQKQOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
Db 61 DSDYDNDDEESMNSPCQVQKQOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHEKG 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 10

US-10-174-654-11
; Sequence 11, Application US/10174654
; Publication No. US20030044937A1

GENERAL INFORMATION:

APPLICANT: Bienkowski, Michael J

Mills, Cynthia J

Jones, David A

TITLE OF INVENTION: TNF-Related Death Ligand

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pharmacia & Upjohn, Intellectual Property

Legal Services

STREET: 301 Henrietta Street

CITY: Kalamazoo

STATE: MI

COUNTRY: USA

ZIP: 49001

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/10/174,654

APPLICATION NUMBER: US/10/174,654

FILING DATE: 19-Jun-2002

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kerber, Lori L.

REGISTRATION NUMBER: 41,113

REFERENCE/DOCKET NUMBER: 6111.N CNI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 616/833-0974

TELEFAX: 616/833-8897

TELEX: 224401

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-174-654-11

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELLKOMODKXSKGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELLKOMODKXSKGIACFLKE 60
Qy 61 DSDYDNDDEESMNSPCQVQKQOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
Db 61 DSDYDNDDEESMNSPCQVQKQOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHEKG 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 11

US-10-151-882-41
; Sequence 41, Application US/10151882
; Publication No. US20030059862A1

GENERAL INFORMATION:

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

FILE REFERENCE: PF554

CURRENT APPLICATION NUMBER: US/10/151,882

CURRENT FILING DATE: 2002-05-22

PRIOR APPLICATION NUMBER: 60/293,100

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin version 3.0

SEQ ID NO 41

LENGTH: 281

TYPE: PRT

ORGANISM: Homo sapiens

US-10-151-882-41

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELLKOMODKXSKGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCVLIVIFTVLLQSLCAVATVYVFTNELLKOMODKXSKGIACFLKE 60
Qy 61 DSDYDNDDEESMNSPCQVQKQOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
Db 61 DSDYDNDDEESMNSPCQVQKQOLRQVLRKMLRTSEETISTVOEKQONISPLVERGPQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSSGHSFLSNLRLNGELVIHEKG 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPPDILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 12

US-10-218-547-20
; Sequence 20, Application US/10218547
; Publication No. US20030100074A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel

```

; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-218-547-20
```

```
Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAMMEVGGPSLGGTCVLIVFTVLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIVFTVLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCQVQKQLRQLVKMLRTSEETISTVOEKQONISPLVERGPO 120
DB 61 DSYWDPNDEESMNSPCQVQKQLRQLVKMLRTSEETISTVOEKQONISPLVERGPO 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRNGLVIHKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRNGLVIHKG 180
QY 181 FYYISQTFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYYISQTFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
```

```

RESULT 13
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF565
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72
```

```
Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
```

```

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCVLIVFTVLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIVFTVLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCQVQKQLRQLVKMLRTSEETISTVOEKQONISPLVERGPO 120
DB 61 DSYWDPNDEESMNSPCQVQKQLRQLVKMLRTSEETISTVOEKQONISPLVERGPO 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRNGLVIHKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRNGLVIHKG 180
QY 181 FYYISQTFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
DB 181 FYYISQTFRFOEIKENTKNDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
```

```

RESULT 14
US-10-139-785-66
; Sequence 66, Application US/1039785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-66
```

```
Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAMMEVGGPSLGGTCVLIVFTVLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCVLIVFTVLQSLCAVATVYVFTNELKQMDKXSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCQVQKQLRQLVKMLRTSEETISTVOEKQONISPLVERGPO 120
DB 61 DSYWDPNDEESMNSPCQVQKQLRQLVKMLRTSEETISTVOEKQONISPLVERGPO 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRNGLVIHKG 180
```

```
Db      121 RVAAHITGRGSRNTLSSPNSKNEKALGKINSWESSRSGHSPNLNHLRNGELVIHEKG 180
Qy      181 FYIYSQTYFRFOEBIKENTKNDKQVQIYKYTSYPPDILMKSARNSCSKDAEYGLY 240
Db      181 FYIYSQTYFRFOEBIKENTKNDKQVQIYKYTSYPPDILMKSARNSCSKDAEYGLY 240
Qy      241 SIYOGIFELKENDRIFVSVTNEHLIDMDHSAFPGAFVVG 281
Db      241 SIYOGIFELKENDRIFVSVTNEHLIDMDHSAFPGAFVVG 281
```

RESULT 15

```
US-10-310-793-26
; Sequence 26, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jlan
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; FILE REFERENCE: PFS73
; CURRENT APPLICATION NUMBER: US/10/310,793
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-310-793-26
```

Query Match 100.0%; Score 1478; DB 14; Length 281;

Best Local Similarity 100.0%; Pred. No. 1,2e-128;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MAMMEVQGGPSLIGQTCVLIVITVLQSLCAVATYYFPTNELKQMDKYSKSGIACFLKE 60
Db      1 MAMMEVQGGPSLIGQTCVLIVITVLQSLCAVATYYFPTNELKQMDKYSKSGIACFLKE 60
Qy      61 DSYMDPNDSESMSPCQVQKQOLVVRKMTLRTSEETISTVOEKQONISPLVREGRPO 120
Db      61 DSYMDPNDSESMSPCQVQKQOLVVRKMTLRTSEETISTVOEKQONISPLVREGRPO 120
Qy      121 RVAAHITGRGSRNTLSSPNSKNEKALGKINSWESSRSGHSPNLNHLRNGELVIHEKG 180
Db      121 RVAAHITGRGSRNTLSSPNSKNEKALGKINSWESSRSGHSPNLNHLRNGELVIHEKG 180
Qy      181 FYIYSQTYFRFOEBIKENTKNDKQVQIYKYTSYPPDILMKSARNSCSKDAEYGLY 240
```

```
Db      181 FYIYSQTYFRFOEBIKENTKNDKQVQIYKYTSYPPDILMKSARNSCSKDAEYGLY 240
Qy      241 SIYOGIFELKENDRIFVSVTNEHLIDMDHSAFPGAFVVG 281
Db      241 SIYOGIFELKENDRIFVSVTNEHLIDMDHSAFPGAFVVG 281
```

Search completed: March 2, 2005, 15:03:07

Job time : 144 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 14:40:57 ; Search time 48 Seconds
(without alignments)
563.269 Million cell updates/sec

Title: US-10-077-435-1
Perfect score: 1478
Sequence: 1 MAMMEVGGPSLIGTQCVLIV.....NEHLIDMDHEASFGAFVLVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 189.5 | 12.8 | 279 | 2 A53062 | Fas ligand - mouse |
| 2 | 186 | 12.6 | 281 | 2 I38707 | Fas ligand - human |
| 3 | 177.5 | 12.0 | 278 | 2 A49266 | Fas ligand - rat |
| 4 | 164 | 11.1 | 261 | 2 S53090 | CD40 ligand - bovl |
| 5 | 147.5 | 10.0 | 261 | 2 I53476 | CD40 ligand - huma |
| 6 | 141 | 9.5 | 234 | 1 A25451 | tumor necrosis fac |
| 7 | 141 | 9.5 | 260 | 1 S21738 | CD40 ligand - mous |
| 8 | 134.5 | 9.1 | 204 | 1 S17289 | tumor necrosis fac |
| 9 | 133 | 9.0 | 232 | 1 S12606 | tumor necrosis fac |
| 10 | 131.5 | 8.9 | 233 | 1 S22052 | tumor necrosis fac |
| 11 | 131 | 8.9 | 234 | 1 J01344 | tumor necrosis fac |
| 12 | 130.5 | 8.8 | 233 | 1 S24642 | tumor necrosis fac |
| 13 | 129.5 | 8.8 | 235 | 1 I54490 | tumor necrosis fac |
| 14 | 127.5 | 8.6 | 204 | 1 S24641 | lymphotoxin - bovl |
| 15 | 125.5 | 8.5 | 233 | 1 QMHUN | tumor necrosis fac |
| 16 | 123.5 | 8.4 | 235 | 1 QMMSN | tumor necrosis fac |
| 17 | 123.5 | 8.4 | 235 | 2 J00029 | tumor necrosis fac |
| 18 | 122 | 8.3 | 205 | 1 QMHUX | lymphotoxin alpha |
| 19 | 121 | 8.2 | 234 | 1 JH0529 | tumor necrosis fac |
| 20 | 115.5 | 7.8 | 193 | 2 S06192 | tumor necrosis fac |
| 21 | 114 | 7.7 | 202 | 1 B27303 | tumor necrosis fac |
| 22 | 113.5 | 7.7 | 185 | 2 S52715 | tumor necrosis fac |
| 23 | 113.5 | 7.7 | 306 | 2 I49139 | lymphotoxin-beta - |
| 24 | 112.5 | 7.6 | 638 | 1 QCBY2M | mRNA meturase b14 |
| 25 | 111.5 | 7.5 | 202 | 1 JN0869 | tumor necrosis fac |
| 26 | 109 | 7.4 | 652 | 2 I48083 | amphotropic murine |
| 27 | 107 | 7.2 | 197 | 1 JH0309 | tumor necrosis fac |
| 28 | 102 | 6.9 | 244 | 2 A46066 | lymphotoxin beta - |
| 29 | 100 | 6.8 | 865 | 2 AB1658 | probable membrane |

| | | | | | |
|----|------|-----|------|----------|---------------------|
| 30 | 99.5 | 6.7 | 233 | 2 S11688 | tumor necrosis fac |
| 31 | 97.5 | 6.6 | 448 | 2 P95122 | protein kinase, pr |
| 32 | 95 | 6.4 | 345 | 2 T14707 | DNA ligase homolog |
| 33 | 95 | 6.4 | 365 | 2 T15010 | hypothetical prote |
| 34 | 95 | 6.4 | 455 | 2 G95104 | hypothetical prote |
| 35 | 94.5 | 6.4 | 4981 | 2 T18489 | hypothetical prote |
| 36 | 94 | 6.4 | 1465 | 2 T23056 | chromodomain helic |
| 37 | 92.5 | 6.3 | 833 | 1 A31593 | heat shock transcr |
| 38 | 92.5 | 6.3 | 1538 | 2 T29095 | cardiac muscle fac |
| 39 | 91 | 6.2 | 1176 | 2 JN0583 | myosin-light-chain |
| 40 | 90.5 | 6.1 | 502 | 2 UC2491 | serine/threonine k |
| 41 | 90.5 | 6.1 | 502 | 2 A53444 | activin receptor-1 |
| 42 | 90.5 | 6.1 | 1284 | 2 T40578 | hypothetical prote |
| 43 | 90 | 6.1 | 907 | 2 E96636 | hypothetical prote |
| 44 | 89.5 | 6.1 | 313 | 2 T03031 | NBS-LRR type resis |
| 45 | 89 | 6.0 | 328 | 2 B59296 | alpha-N-arabino fur |

ALIGNMENTS

```
RESULT 1
A53062
Fas ligand - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A53062
R:Takehashi, T.; Tanaka, M.; Brennan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A>Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A:Reference number: A53062; MUID:94185175; PMID:7511063
A:Accession: A53062
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-279 <TAK>
A:Cross-references: UNIPROT:P41047; GB:U06948; NID:9473564; PIDN:AA17800.1; PID:9473565

Query Match
Best Local Similarity 12.8% Score 189.5; DB 2; Length 279;
Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

QY 83 QLRQLVRKMLRTSETISTVQEKQONISPLVRERGPORVAHAITGTGRSNTLSSPNSK 142
DB 111 ELREFTNQSL-----KVSSEFKQIANPSTPEKKEPSV-AHLTG-----NPSHR 154

QY 143 NEKALGRKINSWESSRSGHFLSNLHNGELVHEKGFYIYSGTFRPFQETENTKN 202
DB 155 SIPL-----EWEDT-YGTALISGVKKKGGLVNETGLVYFYSKYFRGQ-----SCN 201

QY 203 DKQWQYIY-KTYSYDPDILMLKSKAR-NSCWSKDAEYGLYSIYGGIFELKENDRIFVS 260
DB 202 NQPLNHKVMKRSKYPEDLVLMEEKRLNYCTT--CQIWAHSYLGAVENLISADHLIYNI 259

QY 261 TNEHLIDMDHEASFGAF 278
DB 260 SGLSLINFEBSKTFRGV 277

RESULT 2
138707
Fas ligand - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: 138707; J02340; S57565; 138554
R:Takehashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A>Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A:Reference number: 138707; MUID:95127560; PMID:7826947
A:Accession: 138707
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-281 <RES>
A:Cross-references: UNIPROT:P48023; EMBL:U11821; NID:9595430; PIDN:AA50124.1; PID:95954
```

R.Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A>Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A'Reference number: JG2340; MUID:95071350; PMID:7980502
A'Accession: JG2340
A'Molecule type: DNA
A'Residuals: 1-281 <MT>
A'Cross-References: GB:D38122; DDBJ:D29820; NID:G601892; PIDN:BA07320.1; PID:g1369902
R.Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A'Reference number: S57565
A'Accession: S57565
A>Status: preliminary
A'Molecule type: mRNA
A'Residuals: 1-281 <SCH>
A'Cross-References: EMBL:X89102; NID:G887455; PID:G887456
R.Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Gc J. Exp. Med. 181, 71-77, 1995
A>Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A'Reference number: 138554; MUID:95105731; PMID:7528780
A'Accession: 138554
A>Status: preliminary; translated from GB/EMBL/DDBJ
A'Molecule type: mRNA
A'Residuals: 1-281 <RE2>
A'Cross-References: EMBL:U08137; NID:G624627; PIDN:AAC50071.1; PID:G624628
C'Genetics:
A'Gene: FasL
A'Introns: 151/1; 116/3
C'Keywords: glycoprotein; transmembrane protein
F.80-102/Domain: transmembrane #status predicted <TM>
F.76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 186; DB 2; Length 281;
Best Local Similarity 22.1%; Pred. No. 3.4e-08;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

QY 4 MEVGGPSIGQTCVLIIVFTLLQSLCVAV--TYVYFTNELKQMDKYSKSGIACFLKE 60
DB 71 LKRRGNHSTG-LCLVFMFVLVALVGLGFMFOLFKELAELESTSQMHTASLSEK 129
QY 61 DSYNDPNDDESMNSPCQVVKQQLQVVKMLRTSEETISTYQEQQINISLVNERGQ 120
DB 130 QIGHSPPE--KKELRV----- 146
QY 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSMESSRGHSLNLRLNGELVHEKG 180
DB 147 ---ALIT--GKSNRSMP-----LEWEDT-XGIVLSGVKTKGGLVINEG 187
QY 181 FYIYISQTYFRFOEIKENTKDKQVQYIY-KYTSYDPDILMKSAANS-----CWSK 233
DB 188 LYFVYSKYVFRGQ-----SCNNLPLSHKVRNRSKYPODLVMEGKKMSYCTTGQMMAR 241
QY 224 DAEYGLSYTQGIPELKENDRIFFVSYVNEHLIDMDHEASFGAP 278
DB 242 -----SSYLGAVFNLTSGADHLVYVNSLSLVNEESQTFEGLY 279

RESULT 3
A49266
fas ligand - rat
C'Species: Rattus norvegicus (Norway rat)
C'Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C'Accession: A49266
R.Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A>Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A'Reference number: A49266; MUID:94084792; PMID:7505205
A'Accession: A49266
A>Status: preliminary
A'Molecule type: mRNA
A'Residuals: 1-278 <SD>
A'Cross-References: UNIPROT:P36940; GB:U03470; NID:G440178; PIDN:AAC52129.1; PID:G440178
C'Keywords: glycoprotein; transmembrane protein

Query Match 12.0%; Score 177.5; DB 2; Length 278;
Best Local Similarity 27.5%; Pred. No. 1.8e-07;
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

QY 100 ISTVOEKQONISPLVERGQPVAAHITGT-RGRSNTLSSPNSKNEKALGRKINSMESSR 158
DB 121 VSSFEKQJANSTPSETKPKPRSV-AHLTGNPFRSISPL-----EWDPT- 162
QY 159 SGHSFLSNLHLRNGELVHEKGFYIYSGTYFRFOEIKENTKDKQVQYIY-KYTSYP 217
DB 163 YGTALISGVTKYKGGVLINAGLVFVYSKYVFRGQ-----SCNSQPISHKVMENFKYP 216
QY 218 DFILMKSAAR-NSCWSKDAEYGLYSIYQGIPELKENDRIFFVSYVNEHLIDMDHEASFG 276
DB 217 GDLVMEERKUNICYT--GQIWAISSYLGAVFNLTADHLVYVNSISQLINEESKTFPG 274
QY 277 AF 278
DB 275 LY 276

RESULT 4
S53090
CD40 ligand - bovine
C'Species: Bos primigenius taurus (cattle)
C'Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C'Accession: S53090
R.Mertens, B.E.L.C.; Murluki, M.
submitted to the EMBL Data Library, February 1995
A'Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A'Reference number: S53090
A'Accession: S53090
A>Status: preliminary
A'Molecule type: mRNA
A'Residuals: 1-261 <MER>
A'Cross-References: UNIPROT:P51749; EMBL:248469; NID:G732569; PIDN:CAA8363.1; PID:g7325

Query Match 11.1%; Score 164; DB 2; Length 261;
Best Local Similarity 25.9%; Pred. No. 2.3e-06;
Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;

QY 6 VGGPSLQOTCVLIIVFTLL--QSLCVAVTYVFTNELKQMDKYSKSGIACFLKEDDS 63
DB 13 VATGPVSMK-IFMYLLVFLITQWIGSALFAYVLRDLKIEDERNLHEDFVPMK--T 68
QY 64 YMDPNDDESMNS--PCQVVKQQLQVVKMLRTSEETISTYQEQQINISPLVERGQ 121
DB 69 IQRCKRGGSLSLNCBEIRSRFEDLV-KDLMQNR-----VKKEKPMEMHKGQEPQ- 121
QY 122 VAAHITGRGNTLSSPNSKNEKALGRKINSMESSRGHSLSN--LHLRNG-ELVTHE 178
DB 122 IAAHV-----ISEASSKTTSL-----QW-APKGYITLSNNLVTLNKGKDLAVKR 165
QY 179 KGFYIYISQTYFRFOEIKENTKDKQVQYIYKYTSYDPDILMKSAANSWSKDAEYG 238
DB 166 QGFYIYIQTVFCNSNR-----TLGAPPIASLCLSPGSEIRILLRANHTSSKPC--G 219
QY 239 LYSIYQGIPELKENDRIFFVSYVNEHLIDMDHEASFG 276
DB 220 QQSILHGGVFELOGASVFNVTDPDSQVSHGTGTFSG 257

RESULT 5
I53476
CD40 ligand - human
N'Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C'Species: Homo sapiens (man)
C'Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C'Accession: S28017; JH0793; S26594; S28852; I53476; S25684; S30593
R.Hollenbaugh, D.; Grosmaire, L.S.; Kullaa, C.D.; Chalupny, N.J.; Breesch-Andersen, S.;
EMBO J. 11, 4313-4321, 1992
A>Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for

A:Reference number: S28017; MUID:93049181; PMID:1385114
A:Accession: S28017
A:Molecule type: mRNA
A:Residues: 1-261 <HOL>
A:Cross-references: UNIPROT:p29695; EMBL:Z15017; NID:g38483; PIDD:CAA78737.1; PID:g38484
R:Spr:1999, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
J. Exp. Med. 176, 1543-1550, 1992
A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin
A:Reference number: JH0793; MUID:93094757; PMID:1281209
A:Accession: JH0793
A:Molecule type: mRNA
A:Residues: 1-261 <SPR>
A:Cross-references: GB:X67878; NID:g38411; PIDD:CAA8077.1; PID:g38412
A:Experimental source: peripheral blood T-cell
R:Grif, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroccek, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A:Reference number: S26694; MUID:93076854; PMID:1280226
A:Accession: S26694
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <GRA>
A:Cross-references: EMBL:X68550; NID:g37269; PIDD:CAA6554.1; PID:g31270
R:Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Lile, P.; Tomotte, T.; Elsen, G.; Bonnefoy, J.
FEBS Lett. 315, 259-266, 1993
A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
A:Reference number: S28852; MUID:93138085; PMID:7678552
A:Accession: S28852
A:Molecule type: mRNA
A:Residues: 1-261 <GAU>
A:Cross-references: EMBL:L07414; NID:g180123; PIDD:AAA5662.1; PID:g180124
A:Note: The sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
A:Genetics:
A:Gene: GDB:CD40LG; HIGM1; IMD3
A:Cross-references: GDB:120632; OMIM:308230
A:Map position: Xq26-Xq26
C:Keywords: glycoprotein; transmembrane protein
F:13-44/Domain: transmembrane #status predicted <TM>
F:45-261/Domain: extracellular #status predicted <EXT>
F:6/240/Binding site: carbohydrate (Asn) (covalent) #status predicted

| Query Match | 10 0% | Score 147.5 | DB 2 | Length 261 |
|-----------------------|-------|---|---------------|------------|
| Best local Similarity | 23.7% | Pred. No. 5.7e-05 | | |
| Matches | 66 | Conservative 51 | Mismatches 99 | Indels 63 |
| | | | Gaps 15 | |
| QY | 17 | VLIVIFVYL--QSLCAVAVTVYFTNELKQMDKYSKGIACFLKEDSDYMDP-----ND | 69 | |
| DB | 23 | IFWLLITVFLITOMGSLFAVYLRRLDKIEDEN-----LHEDVVPKTIORCNTG | 75 | |
| QY | 70 | EESNN-SPCQVQKWLRLVRKMLIRTSSEITISVQEKQONISPLVRERGPQVAHITG | 128 | |
| DB | 76 | ERSLILNCEIKSQPEGFVKDML-NKEET-----KKNSPEWKGQNPQ-IAAHV-- | 126 | |
| QY | 129 | TRGRNNTLSSPNKSKKELGKRKINWESSRSQSHSLN--LHLRNG-ELVHEKGFYIT | 185 | |
| DB | 127 | -----ISEASSKITSVL-----QW--AEKQYTMNSKQLTVLENGKQLTVKQGLYYIT | 172 | |
| QY | 186 | SQTVRFPQBEIKENT-----KNDKQWQVQIYKYTSYPPDILMKSGARNSCSKDAEY | 237 | |
| DB | 173 | KQVTCNSNRKASSQAPFLASLCLKSPGRFR-----ILRPAANTHSSAKPC-- | 218 | |
| QY | 238 | GLYSIVQGIPELKENDRIPVSVTNEHLIDMDHEASFFG | 276 | |
| DB | 219 | GGQSIHLGVSFELQPGASVFVWVTDPSQVSHOTGTSFG | 257 | |

RESULT 6
A25451
tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A25454; A25451; J50727

R.Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.
 DNA 5, 149-156, 1986
 A>Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for, rat
 A.Reference number: A25454; MUID:66219711; PMID:3519137
 A:Accession: A25454
 A:Molecule type: mRNA
 A:Residues: 1-234 <IT0>
 A:Cross-references: UNIPROT:P04924; GB:M12845; NID:G165759; PIDN:AAA31486.1; PID:G165760
 R.Ito, H.; Shirai, T.; Yamamoto, S.; Akita, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
 DNA 5, 157-165, 1986
 A>Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
 A.Reference number: A25451; MUID:66219712; PMID:3519138
 A:Accession: A25451
 A:Molecule type: DNA
 A:Residues: 1-234 <IT2>
 A>Note: this sequence differs from that shown in having a Gln inserted between residues
 R.Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
 Gene 95, 215-221, 1990
 A>Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF
 A.Reference number: JH0309; MUID:91065534; PMID:2249779
 A:Accession: J50727
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-62, 'Q', 63-234 <SHA>
 A:Cross-references: GB:M60340; GB:M35326; NID:G165754; PIDN:AAA31484.1; PID:G165756
 A:Genetics:
 A:Insertions: 62/3; 80/1; 96/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cyclooxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
 F.1-81/Domain: propeptide #status predicted <PRO>
 F.82-234/Product: tumor necrosis factor #status predicted <MAT>
 F.119/20/Binding site: myristate (lys) (covalent) #status predicted
 F.83/Binding site: carbonylate (Ser) (covalent) #status predicted
 F.147-178/Dissulfide bonds: #status predicted

Query Match 9.5%; Score 141; DB 1; Length 234;
 Best local similarity 22.4%; Pred. No. 0.00017;
 Matches 62; Conservative 41; Mismatches 98; Indels 76; Gaps 13;

| | | | |
|----|-----|---|-----|
| Oy | 8 | GGPSLQGTCLVLIIVITVLLQSLCAVATVTVVFTNELKQMODKYSKSGIACFLKEDDSYWP | 67 |
| Db | 22 | GGPGSKRCICLCLSLFSFL-----VAGATTLF-----CLL--HFRVIGP | 58 |
| Oy | 68 | NDEESMNSPCMQVKKQLRQLYRKMI-LRTSEBITSTVOEKQONISPLVREBGFQVAAH | 126 |
| Db | 59 | QEEBSPPNN-----LHLVNPVACQVTLRSASRALSD-----KPL-----AHV | 94 |
| Oy | 127 | TGTRGRNTLSSPNSKNEKKLGRKINWESRSCHSLNHLRNGELVYHEKGFYYIS | 186 |
| Db | 95 | VA-----NPVEGQL-----QWLSQRAAALLIANGKCLTDNLVVPADGLYIIS | 138 |
| Oy | 187 | QTYRPOBEIKENTKNQKQWQVYIKY-TSYDPDILMLKSARNSCWSDAEYG-----LY | 240 |
| Db | 139 | QVLFESGQ-----GGRSVLLLTHYSRFAVYENKNVNLISAKSCHETFBEMAPMAWE | 193 |
| Oy | 241 | SIYGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG | 276 |
| Db | 194 | PVILGVFQLEKGDRLSTEVNQPEYLDLAESGQYFFG | 230 |

RESULT 7
 S21738
 CD40 ligand - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: S21738
 R:Armstrong, R.J.; Farnlow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.
 Nature 357, 80-82, 1992
 A>Title: Molecular and biological characterization of a murine ligand for CD40.
 A:Reference number: S21738; MUID:92244364; PMID:1374155
 A:Accession: S21738
 A:Molecule type: mRNA

Db 182 EGAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 228

RESULT 10

tumor necrosis factor alpha precursor - baboon

C/Species: Papio sp. (baboon)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: S22052

R/Sanjana, M.; Edwards, A.

submitted to the EMBL Data Library, September 1991

A/Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A/Reference number: S22052

A/Accession: S22052

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-233 <SAS>

A/Cross-references: UNIPROT:P33620; EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160

C/Genetics:

A/Introns: 62/3; 78/1; 94/1

C/Superfamily: tumor necrosis factor

C/Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F/19/20/Binding site: myristate (Lys) (covalent) #status predicted

F/81/Binding site: carbonylate (Ser) (covalent) #status predicted

F/145-177/Dissulfide bonds: #status predicted

Query Match 8.9%; Score 131.5; DB 1; Length 233;

Best Local Similarity 19.2%; Pred. No. 0.0011;

Matches 55; Conservative 49; Mismatches 98; Indels 85; Gaps 10;

Db 2 AMMEVGGPSLQGTCLVLIPTVLQSLCAVAVYVYFTNELKQMDKSKSGIACFLKED 61

16 ALPKRTGPGQSRRLFLSFLSLVAGATTLFCLHGVIPQGEPPK----- 65

62 DSYMDPNDSESNMSPCQVQKQLRQLVRKMLRTSEETISTVQEQONISPLVRERGP 121

66 ----DF-----SLISPLAQ-----VRSSSRPS-----DK 87

122 VAAHTTGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVHIEKGF 181

88 PVAHVVA-----NPAEQGL--QMLNRNALANGLVETLRDQLVPSRGL 131

182 YIYSQTFRFOEIKENTKNDKQVQIYKYT-----SYDPILLMKSARNSCWSK-- 233

132 YLISQVLFKQ-----GCPSTHYLLTHTISRLAVSYTKNLSAITSPPQRETP 182

234 ---DAEYGLYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

183 EGAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 229

Db 183 EGAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 229

234 ---DAEYGLYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

183 EGAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 229

Db 183 EGAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 229

234 ---DAEYGLYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

183 EGAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 229

Db 183 EGAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 229

234 ---DAEYGLYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

F/19/20/Binding site: myristate (Lys) (covalent) #status predicted

F/82/Binding site: carbonylate (Ser) (covalent) #status predicted

F/146-178/Dissulfide bonds: #status predicted

Query Match 8.9%; Score 131; DB 1; Length 234;

Best Local Similarity 20.8%; Pred. No. 0.0012;

Matches 60; Conservative 40; Mismatches 89; Indels 100; Gaps 13;

Db 8 GGPISLQGTCLVLIPTVLQSLCAVAVYVYFTNELKQMDKSKSGIACFL-----X 59

22 GGPQSRRLCLTSLFSL-----VAGATTLF-----CLHFGVIGPQR 60

60 EDDSYMDPNDSESNMSPCQVQKQLRQLVRKMLRTSEETISTVQEQONISPLVRERGP 119

61 ESQL--PNAFQSLN-PLAQ-----LRSSSRPS----- 86

120 QVAAHTTGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVHIEK 179

87 DKPVAHVVA-----NPAEQGL--QMLSGRANALLANGVLTGNDLVLPD 130

180 GPYIYSQTFRFOEIKENTKNDKQVQIYKYT-----SYDPILLMKSARNSCWSK 233

131 GLYIYSQVLFKQ-----GCPSTHYLLTHTISRLAVSYTKNLSAITSPPQRETP 181

234 DAEV-----LYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

Db 182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

234 DAEV-----LYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

Db 182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

234 DAEV-----LYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

Db 182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

234 DAEV-----LYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

Db 182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

234 DAEV-----LYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

Db 182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

234 DAEV-----LYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

Db 182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

234 DAEV-----LYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

Db 182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

234 DAEV-----LYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

Db 182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

234 DAEV-----LYSIYOGIFELKENDRIFVSVTNEHLIDMDHEAS-FPG 276

182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

Db 182 SPEQAEKPMWEPYILGCVFQLEKDRLSAEINLPDYLDFAESGQVYFG 230

QY 231 ---MSKDAEGLYSTYGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
Db 181 TPENVA-EAKPWYEPITYGGVFOLEKGRDLSEAINLPDYLDVAESQVYFG 229
RESULT 13
154490
tumor necrosis factor alpha precursor - white-footed mouse
C:Species: Peromyscus leucopus (white-footed mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: 154490
R:Crew, M.D.; Filipowaky, M.E.
Immunogenetics 35, 351-353, 1992
A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leu
A:Reference number: 154490; MUID:92218012; PMID:1348497
A:Accession: 154490
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: UNIPROT:P36939; GB:M59233; NID:G202506; PIDN:AAA40596.1; PID:G202507
C:Genetics:
A:Gene: P1TNF
A:Introns: 62/3: 81/1: 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation
F:19/20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carboxylate (Ser) (covalent) #status predicted
Query Match 8.8%; Score 129.5; DB 2; Length 235;
Best Local Similarity 24.5%; Pred. No. 0.0016; Indels 25; Gaps 9;
Matches 45; Conservative 39; Mismatches 75;
QY 110 ISPLVRRGPPORVAHITGTGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSQH 161
Db 56 IGPQREKEFPNNLP--IIGSMAQTLTLRSSSGNSDKPVAAHVAAHQVDEQLEMTSRGAN 113
QY 162 SFLSN-LHRLNGELVYHEKGFYIYSQTYFRFOEIKENTKDKQKVQYIYK-TSYDP 219
Db 114 ALLANGMDLKNQVLPADGLTVYSQVLFKQ-----GCSSTYVLLTHIVSRFAVSDEPK 168
QY 220 ILLMSANSCWSCSKDAEY-----LYSYGGIFELKENDRIFVSVTNEHLIDMDHEAS 273
Db 169 VNLISAIRSPC-PKSTPGRSELKPWYEPITYLGGVFOLEKGRDLSEAVMLPKYLDPAESGQ 227
QY 274 -FFG 276
Db 228 VYFG 231
RESULT 14
S24641
lymphotoxin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: I46046; S24641
R:Cludts, I.; Cleuter, Y.; Keltmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
A:Reference number: I46046; MUID:94083525; PMID:8260599
A:Accession: I46046
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-204 <CL2>
A:Cross-references: UNIPROT:Q06600; EMBL:Z14137; NID:g796; PIDN:CAA76510.1; PID:g797
C:Genetics:
A:Introns: 32/3; 68/1
C:Superfamily: tumor necrosis factor
Query Match 8.6%; Score 127.5; DB 1; Length 204;
Best Local Similarity 24.9%; Pred. No. 0.002; Indels 35; Gaps 9;
Matches 47; Conservative 29; Mismatches 78;
QY 99 TISTVQEKQNIISPLVRRGPPORVAHITG-----TRGRSNTLSSPNSKNEKALGRKI 151

Db 40 TPSSAQPAAQOL-PPPTFRGTLPKPAALVGPSTDSLRWANT-----DRAFLR-- 88
QY 152 NSWESSRSGHSFSLNLRNGELVYHEKGFYIYSQTYFRFOEIKENTKDKQKVQYIY 211
Db 89 -----HGF-----SLSNSLIVPTSGLVFVYSQVYFSGRGCRPRATPTPLYLAAHEQ 135
QY 212 KYT-SYDPPIILMSARNSCSKDAEGLYSTYGGIFELKENDRIFVSVTN-EHLIDMD 269
Db 136 LFSFGYPPHVLPLSKQKSCVCPQGPW-VRSVYQCAVFLTRGDQLSTHTDGISSLT-LS 193
QY 270 HEASFFGAF 278
Db 194 PSSVFFGAF 202
RESULT 15
OHMUN
tumor necrosis factor alpha precursor [validated] - human
N:Alternate names: cachectin; TNFA
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
A:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R:Nedwin, G.E.; Naylor, S.L.; Sakauchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D
Nucleic Acids Res. 13, 6361-6373, 1985
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chr
A:Reference number: A93585; MUID:86016093; PMID:2995927
A:Accession: A93585
A:Molecule type: DNA
A:Residues: 1-233 <NED>
A:Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; P
R:Rits, F.J.M.; Bougueleret, L.; Prieux, S.; Caterina, D.; Primas, G.; Perrot, V.; Jukka
Nature Genet. 3, 137-145, 1993
A:Title: Dense Alu clustering and a potential new member of the Nfkapab family within a
A:Reference number: S36152; MUID:93272029; PMID:8499947
A:Accession: S36153
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-233 <IR1>
A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A:Title: Human tumor necrosis factor: precursor structure, expression and homology to 1
A:Reference number: A93351; MUID:85086244; PMID:6392892
A:Accession: A93351
A:Molecule type: mRNA
A:Residues: 1-233 <PRN>
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A>Note: This protein was isolated from the monocyte-like cell line HL-60 from a promyelo
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.;
Science 228, 149-154, 1985
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A:Reference number: A44189; MUID:85142190; PMID:3856324
A:Accession: A44189
A:Molecule type: mRNA
A:Residues: 1-62, 'S', 'G', '64-233 <WAN>
A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
Lymphokine Res. 7, 175-185, 1988
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A:Reference number: A61478; MUID:88301617; PMID:2841543
A:Accession: B61478
A:Molecule type: protein
A:Residues: 83-102;109-119;121-128, 'X',130-131;142-144, 'X',146, 'XXX',150-152;159-174;180
R:Marmonou, A.; Franssen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1985
A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A:Reference number: I53311; MUID:86030296; PMID:3932069
A:Accession: I53311
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-233 <MAR>

A:Cross-references: GB:M26331; NID:G339763; PIDN:AAA36758.1; PID:G339764
A:Experimental source: U-937 cells
R:Takekura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A:Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A:Reference number: S62610; MUID:96202967; PMID:8631363
A:Accession: S62610
A:Molecule type: protein
A:Residues: 77-99 <TAK>
R:D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter region
A:Reference number: I54522; MUID:94102809; PMID:7903959
A:Accession: I54522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <DAL>
A:Cross-references: GB:S68530; NID:G544751
R:Stevenson, F.T.; Bureten, S.L.; Lockaley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine
A:Reference number: A59165; MUID:93018820; PMID:1402651
A:Contents: annotation; identification of myristylated lysines
R:Aggarwal, B.B.; Kohr, W.J.; Haas, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Brink
J. Biol. Chem. 260, 2345-2354, 1985
A:Title: Human tumor necrosis factor. Production, purification, and characterization.
A:Reference number: A92511; MUID:8510974; PMID:3871770
A:Contents: annotation; disulfide bond
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
out detriment to normal cells. It can also act synergistically with interferon gamma to
C:Comment: TNF-alpha and -beta (lymphocytin) are the products of different genes closely
related and are produced by different cell types and have different induction kinetics.
C:Genetics:
A:Gene: GDB:TNF, TNFA
A:Cross-references: GDB:120441; OMIM:191160
A:Map position: 6p21.3-6p21.3
A:Introns: 62/3; 78/1; 94/1
C:Complex: homotrimer
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxic; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage
F:1-76/Domain: propeptide #status predicted <PRO>
F:77-233/Product: tumor necrosis factor #status experimental <MAT>
F:19, 20/Binding site: myristate (Lys) (covalent) #status experimental
F:81/Binding site: carbohydrate (Ser) (partial) #status experimental
F:145-177/Disulfide bonds: #status experimental

Query Match 8.5%; Score 125.5; DB 1; Length 233;
Best Local Similarity 17.8%; Pred. No. 0.0036;
Matches 51; Conservative 52; Mismatches 99; Indels 85; Gaps 9;

QY 2 AMMEVOGPGSLGCTCYLVIFVTVLQSLCVAVTVYFTNELKQMODKSKSGIACFLKED 61
DB 16 ALPKKTGGQGRSRLCLFSLFSLVAGATTLFCILHFGVIGPQREFFPR----- 65
QY 62 DSYMPDNDESNMSPQWQKQRLQRLVRKMLRTSEETISTVQEKQNTSPLVRERGPOR 121
DB 66 -----DLSLISPLAQ-----VRSSSRTPS-----DK 87
QY 122 VAAHITGTRGRNLTSSPNSKNEKALGRKINSMESSRSGHSLSLNLHNGELVYHEKGF 181
DB 88 PVAHVVA-----NPAEGQL--QWLNRRAVALANGVELADNQLVPSSEGL 131
QY 182 YTIYQGTFRFOBEIKENTKNDKQNVQYIKYT-----SYDPILIMKSARNSCSK-- 233
DB 132 YLIYQVLFKQ-----GCPSTHVLLTHTISRIVASYQTKVNLISAIKSPCORERP 182
QY 234 ---DAEYGLYSIYOGIFELKENDRIFVSTNEHLMDHBA--FRG 276
DB 183 EGAEAKPWTEPIYLGQVFLQEKDRLSAETINRPDYIDPFAESGQVYFG 229

Search completed: March 2, 2005, 14:51:37
Job time : 51 secs

